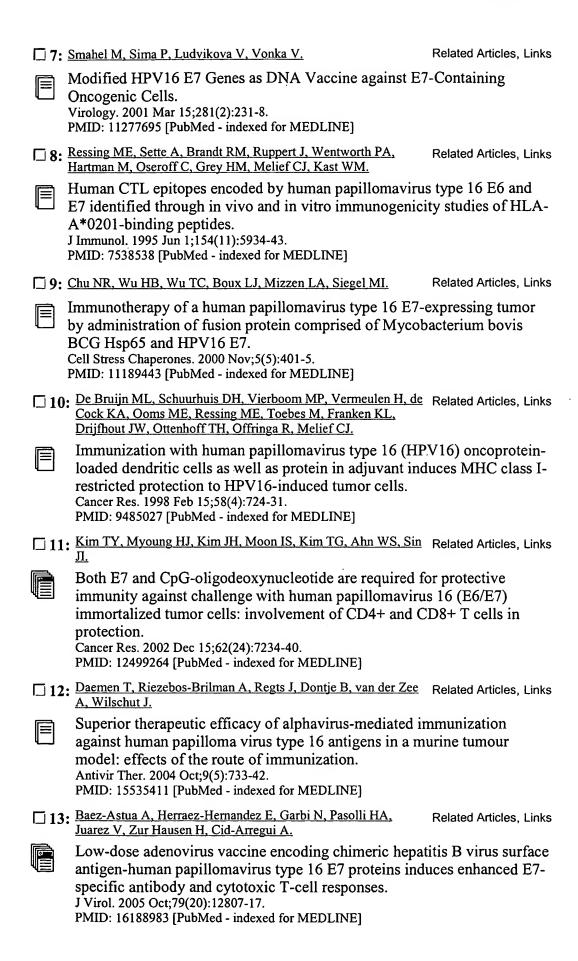
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Entrez PubMed Overview Help FAQ Tutorials New/Noteworthy E-Utilities	□1: [Zhou X, Qian Efficient exp protein and Biol Pharm Bu PMID: 149937	oression of the antitur II. 2004 Ma	f modified nor efficac r;27(3):303-7	human pap y in a mous 7.	se model.		ed Articles e7 fusio			
PubMed Services Journals Database MeSH Database Single Citation Matchel Batch Citation Matcher Clinical Queries Special Queries LinkOut		Genetic immunization against cervical carcinoma: induction of cytotoxic T lymphocyte activity with a recombinant alphavirus vector expressing human papillomavirus type 16 E6 and E7. Gene Ther. 2000 Nov;7(21):1859-66. PMID: 11110419 [PubMed - indexed for MEDLINE]									
My NCBI	□3:	Daemen T, Re	gts J, Holtro	p M, Wilsch	ut J.		Relate	d Articles	, Links		
Related Resources Order Documents NLM Mobile NLM Catalog NLM Gateway TOXNET		Immunization vector expression papillomavingene Ther. 20 PMID: 118570	essing high rus 16 E6 02 Jan;9(2):	n levels of a and E7. 85-94.	a stable fus	ion protei	-				
Consumer Health Clinical Alerts ClinicalTrials.gov	□4:	Pokorna D, Ma Smahel M.	ackova J, Dı	iskova M, Ri	ttich S, Ludv	ikova V,	Relate	d Articles	, Links		
PubMed Central		Combined in papillomavir J Gene Med. 2 PMID: 157123	rus type 16 005 Jun;7(6)	6 did not ei):696-707.	nhance anti	tumor eff	_	e of hun	nan		
	□ 5:	Chu NR, Wu I	łB, Wu T, E	Boux LJ, Sieg	gel MI, Mizze	en LA.	Relate	ed Articles	, Links		
		Immunotherapy of a human papillomavirus (HPV) type 16 E7-expressing tumour by administration of fusion protein comprising Mycobacterium bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7. Clin Exp Immunol. 2000 Aug;121(2):216-25. PMID: 10931134 [PubMed - indexed for MEDLINE]									
	□ 6:	Cassetti MC, N Eiben GL, Sm	AcElhiney S ith LR, Kast	P, Shahabi V WM.	, Pullen JK,	Le Poole IC	Relate	ed Articles	, Links		
		Antitumor e particles end Vaccine. 2004 PMID: 146703	fficacy of coding mu Jan 2;22(3-	Venezuela tated HPV 4):520-7.	16 E6 and 1	E7 genes.	s virus re	plicon			

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□ 14:	Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC.	Related Articles, Links
	Anti-tumor DNA vaccines based on the expression of happillomavirus-16 E6/E7 oncoproteins genetically fuse glycoprotein D from herpes simplex virus-1. Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9. PMID: 16213178 [PubMed - indexed for MEDLINE]	
□ 15:	Sun Q, Tang SC, Pater MM, Pater A.	Related Articles, Links
	Different HPV16 E6/E7 oncogene expression patterns reconstructed from HPV16-immortalized human endoc genital keratinocytes. Oncogene. 1997 Nov 13;15(20):2399-408. PMID: 9395236 [PubMed - indexed for MEDLINE]	_
□ 16:	Azoury-Ziadeh R, Herd K, Fernando GJ, Frazer IH, Tindle RW.	Related Articles, Links
	T-helper epitopes identified within the E6 transforming cervical cancer-associated human papillomavirus type Viral Immunol. 1999;12(4):297-312. PMID: 10630789 [PubMed - indexed for MEDLINE]	•
□ 17:	Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.	Related Articles, Links
	Immunogenicity of dendritic cell-based HPV16 E6/E7 CTL activation and protective effects. Folia Biol (Praha). 2004;50(6):184-93. PMID: 15709713 [PubMed - indexed for MEDLINE]	peptide vaccines:
□ 18:	Fernando GJ, Murray B, Zhou J, Frazer IH.	Related Articles, Links
	Expression, purification and immunological characterizatransforming protein E7, from cervical cancer-associate papillomavirus type 16. Clin Exp Immunol. 1999 Mar;115(3):397-403. PMID: 10193409 [PubMed - indexed for MEDLINE]	
□ 19:	Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.	Related Articles, Links
	Development of a DNA vaccine targeting human papil oncoprotein E6. J Virol. 2004 Aug;78(16):8468-76. PMID: 15280455 [PubMed - indexed for MEDLINE]	lomavirus type 16
□ 20:	Kadish AS, Ho GY, Burk RD, Wang Y, Romney SL, Ledwidge R, Angeletti RH.	Related Articles, Links
	Lymphoproliferative responses to human papillomaviruproteins E6 and E7: outcome of HPV infection and asset J Natl Cancer Inst. 1997 Sep 3;89(17):1285-93. PMID: 9293919 [PubMed - indexed for MEDLINE]	
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Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: CN 1160463 C, CN 1381583 A

L4: Entry 1 of 3

File: DWPI

Aug 4, 2004

DERWENT-ACC-NO: 2003-258260

DERWENT-WEEK: 200612

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TITLE: Human papillomavirus E6/E7 fusion gene and its efficient expression carrier

and fusion protein vaccine

INVENTOR: ZHAO, Q

PRIORITY-DATA: 2002CN-0117143 (April 24, 2002)

PATENT-FAMILY:

 PUB-NO
 PUB-DATE
 LANGUAGE
 PAGES
 MAIN-IPC

 CN 1160463 C
 August 4, 2004
 000
 C12N015/62

 CN 1381583 A
 November 27, 2002
 000
 C12N015/62

INT-CL (IPC): $\underline{A61}$ \underline{K} $\underline{48/00}$; $\underline{A61}$ \underline{P} $\underline{35/00}$; $\underline{C07}$ \underline{K} $\underline{19/00}$; $\underline{C12}$ \underline{N} $\underline{15/62}$; $\underline{C12}$ \underline{N} $\underline{15/63}$

Full Title Citation Front Review Classification Date Reference Seguences Attachments Claims KMC Draw De

Document ID: NZ 505108 A, WO 9933868 A2, AU 9924191 A, ZA 9811848 A, EP 1040123 A2, BR 9814487 A, CZ 200002376 A3, AU 729336 B, HU 200100526 A2, JP 2001527091 W

L4: Entry 2 of 3

File: DWPI

Oct 25, 2002

DERWENT-ACC-NO: 1999-405485

DERWENT-WEEK: 200274

COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce

immune response to HPV

INVENTOR: DALEMANS, W L J; GERARD, C M G

PRIORITY-DATA: 1997GB-0027262 (December 24, 1997)

PATENT-FAMILY:

 PUB-NO
 PUB-DATE
 LANGUAGE
 PAGES
 MAIN-IPC

 NZ 505108 A
 October 25, 2002
 000 A61K039/02

 WO 9933868 A2
 July 8, 1999
 E 062 C07K014/00



Record List Display Page 2 of 3

AU 9924191 A	July 19, 1999		000	
ZA 9811848 A	July 26, 2000		063	C07K000/00
EP 1040123 A2	October 4, 2000	E	000	C07K014/00
BR 9814487 A	October 10, 2000		000	C07K014/00
CZ 200002376 A3	November 15, 2000		000	C07K014/01
AU 729336 B	February 1, 2001		000	C07K014/00
HU 200100526 A2	June 28, 2001		000	A61K039/12
JP 2001527091 W	December 25, 2001		093	C07K014/025

INT-CL (IPC): $\underline{A61}$ K $\underline{38/16}$; $\underline{A61}$ K $\underline{39/00}$; $\underline{A61}$ K $\underline{39/02}$; $\underline{A61}$ K $\underline{39/09}$; $\underline{A61}$ K $\underline{39/102}$; $\underline{A61}$ K $\underline{39/385}$; $\underline{A61}$ K $\underline{39/39}$; $\underline{A61}$ P $\underline{35/00}$; $\underline{C07}$ K $\underline{0/00}$; $\underline{C07}$ K $\underline{14/01}$; $\underline{C07}$ K $\underline{14/025}$; $\underline{C07}$ K $\underline{14/285}$; $\underline{C07}$ K $\underline{14/315}$; $\underline{C07}$ K $\underline{19/00}$; $\underline{C12}$ N $\underline{15/09}$

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Decument ID: DE 69824013 T2, WO 9910375 A2, AU 9892639 A, ZA 9807591 A, NO 200000850 A, EP 1007551 A2, BR 9812139 A, CZ 200000634 A3, CN 1276833 A, HU 200004327 A2, AU 732946 B, MX 2000001813 A1, KR 2001023193 A, JP 2001513986 W, US 6342224 B1, NZ 502632 A, US 20020182221 A1, EP 1007551 B1, DE 69824013 E, ES 2221198 T3

L4: Entry 3 of 3 File: DWPI Jun 2, 2005

DERWENT-ACC-NO: 1999-190587

DERWENT-WEEK: 200537

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TITLE: Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for

treatment or prophylaxis of HPV induced lesions

INVENTOR: BRUCK, C; DELISSE, A E F ; GERARD, C M G ; LOMBARDO-BENCHEIKH, A ; SILVA, T C ; CABEZON, S T ; CABEZON SILVA, T ; FERNANDE DELISSE, A E ; GHISLAINE GERARD, C M

PRIORITY-DATA: 1997GB-0017953 (August 22, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
DE 69824013 T2	June 2, 2005		000	C07K014/025
WO 9910375 A2	March 4, 1999	E	095	C07K014/00
AU 9892639 A	March 16, 1999		000	C07K014/00
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NO 200000850 A	April 14, 2000		000	C07K019/00
EP 1007551 A2	June 14, 2000	E	000	C07K014/00
BR 9812139 A	July 18, 2000		000	C07K014/00
CZ 200000634 A3	January 17, 2001		000	C07K014/00
CN 1276833 A	December 13, 2000		000	C12N015/62
HU 200004327 A2	March 28, 2001		000	C07K014/00
AU 732946 B	May 3, 2001		000	C07K014/00
MX 2000001813 A1	October 1, 2000		000	C07K014/00
KR 2001023193 A	March 26, 2001		000	C12N015/62



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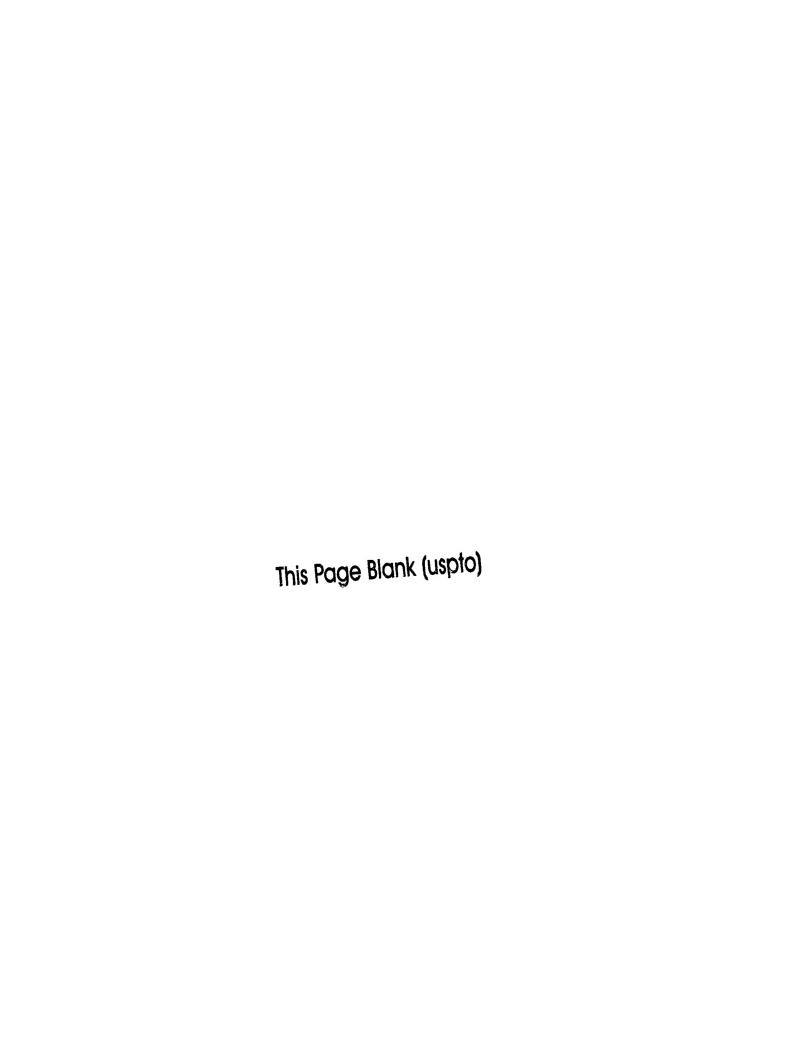
JP 2001513986 W	September 11, 2001		131	C12N015/09
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NZ 502632 A	March 28, 2002		000	C07K014/285
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NZ 502632 A , US 20020182221 A1 INT-CL (IPC): A61 K 9/107; A61 K 38/02; A61 K 39/00; A61 K 39/12; A61 K 39/145; A61 K 39/39; A61 P 35/00; A61 P 37/00; C07 H 14/00; C07 H 21/04; C07 K 0/00; C07 K 1/00; C07 K 14/00; C12 N 1/15; C12 N 1/19; C12 N 1/20; C12 N 1/21; C12 N 1/20; C12 N

Full	Title Citation	Front	Review	Classification	Date	Reference		经常的问题	Claims	KWIC Draw
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Search Results - Record(s) 1 through 6 of 6 returned.

☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants .

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Friede; Martin Court St Etienne BE Hermand; Philippe Court St Etienne BE

US-CL-CURRENT: $\underline{424}/\underline{184.1}$; $\underline{424}/\underline{278.1}$, $\underline{424}/\underline{283.1}$, $\underline{514}/\underline{25}$

Full Title Citation Front Review Classification Date Reference Securities Machineries Claims KMC Draw. Do

☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6 File: USPT Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Friede; Martin Farnham GB

Garcon; Nathalie Wavre BE
Gerard; Catherine Marie Ghislaine Rhode Saint Genese BE
Hermand; Philippe Court-Saint-Etienne BE

US-CL-CURRENT: $\underline{424}/\underline{184.1}$; $\underline{424}/\underline{208.1}$, $\underline{424}/\underline{228.1}$, $\underline{424}/\underline{229.1}$, $\underline{424}/\underline{231.1}$, $\underline{424}/\underline{249.1}$, $\underline{424}/\underline{278.1}$, $\underline{424}/\underline{283.1}$, $\underline{514}/\underline{25}$

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Full Title Citation Front Review Classification Date Reference Sequences Attachments: Claims KWC Draw De

☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Bruck; Claudine	Rixensart				BE
Silva; Teresa Cabezon	Lenkebeek				BE
Fernande Delisse; Anne-Marie Eva	Gosselies				BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese				BE
Lombardo-Bencheikh; Angela	Wavre				BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1, 435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	Stellering	級性的影響的	Claims	KWIC	Draw, De

☐ 4. Document ID: US 6306397 B1

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File: USPT Oct 23, 2001

US-PAT-NO: 6306397

L10: Entry 4 of 6

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME Edwards; Stirling John Northcote AU AU Cox; John Cooper Bullengarook AU Webb; Elizabeth Ann Eltham Frazer; Ian St. Lucia ΑU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7, 536/23.1, 536/23.72, 536/24.3

Full Title Citation Front Review Classification Date Reference Sequences Attachnicals Claims KMC Draw De



☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

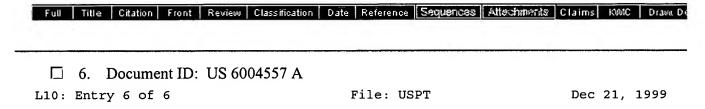
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Webb; Elizabeth AnnElthamAUEdwards; Stirling JohnNorthcoteAU

US-CL-CURRENT: 424/199.1; 424/192.1, 435/235.1, 435/320.1, 435/325, 435/69.1,

<u>435/69.7</u>



US-PAT-NO: 6004557

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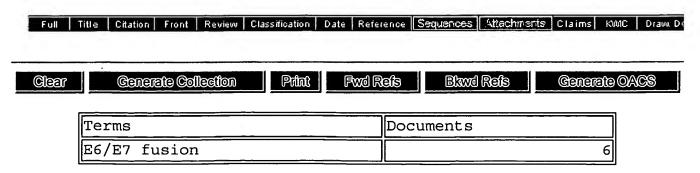
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DATE-ISSUED: December 21, 1999

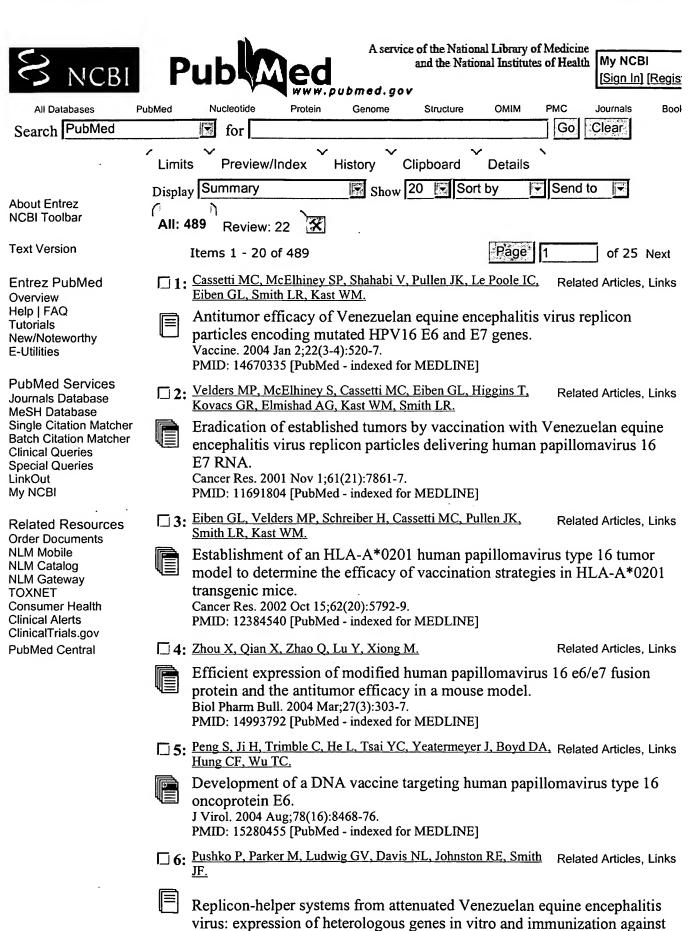
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NAME CITY STATE ZIP CODE COUNTRY

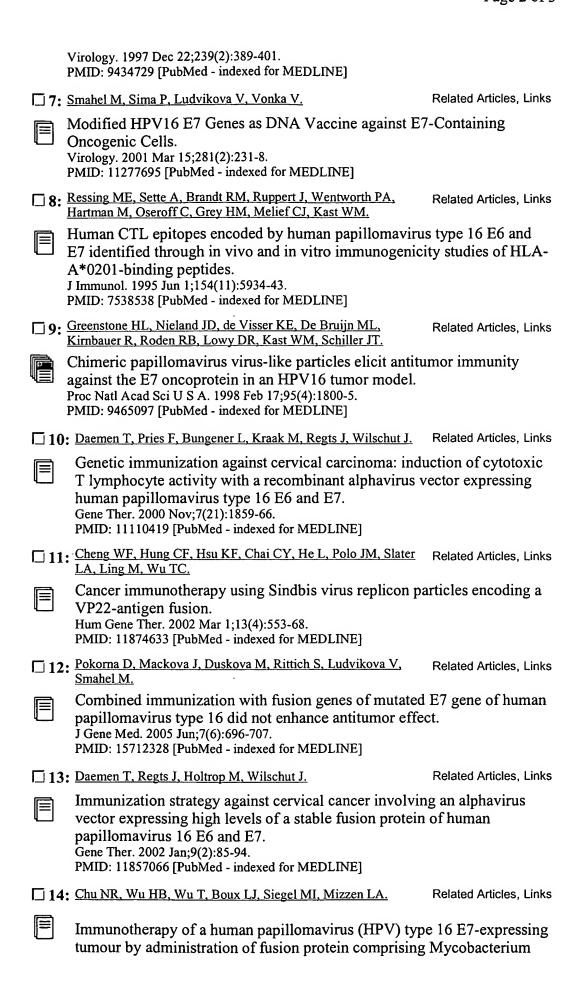
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Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia. AU



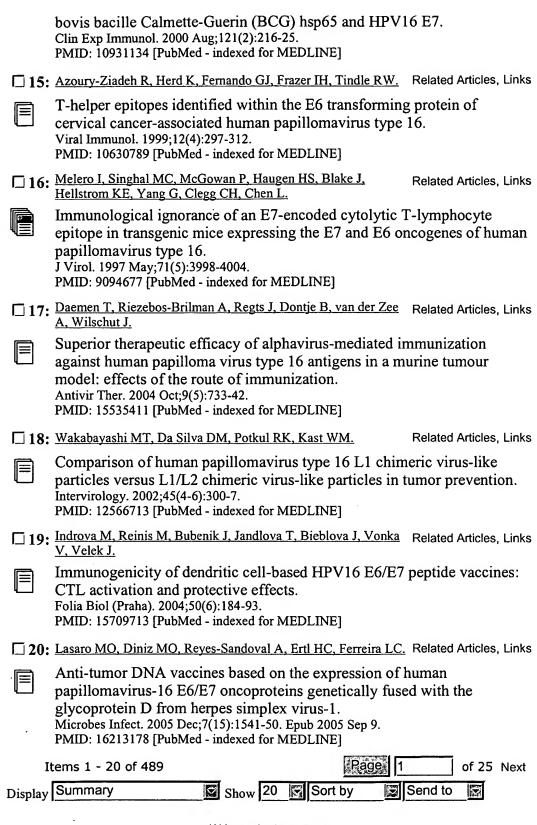
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heterologous pathogens in vivo.



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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6 File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Friede; Martin Court St Etienne BE Hermand; Philippe Court St Etienne BE

US-CL-CURRENT: <u>424/184.1</u>; <u>424/278.1</u>, <u>424/283.1</u>, <u>514/25</u>

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KMC Draw De

☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6 File: USPT Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

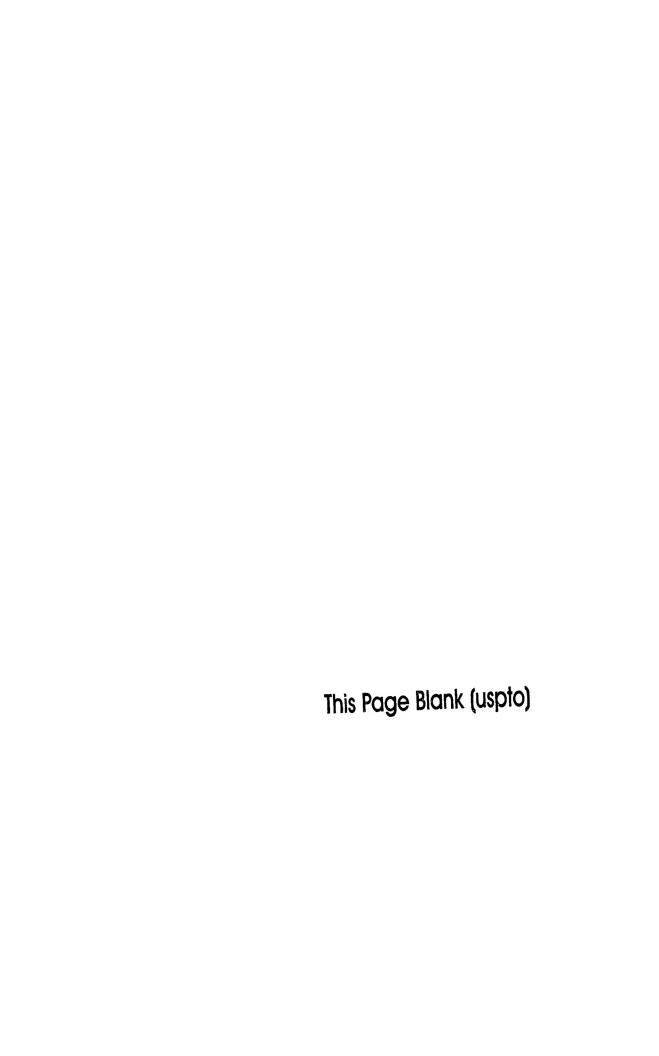
DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Friede; Martin Farnham GB
Garcon; Nathalie Wavre BE
Gerard; Catherine Marie Ghislaine Rhode Saint Genese BE
Hermand; Philippe Court-Saint-Etienne BE

US-CL-CURRENT: 424/184.1; 424/208.1, 424/228.1, 424/229.1, 424/231.1, 424/249.1, 424/278.1, 424/283.1, 514/25



Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw De

☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Bruck; Claudine	Rixensart				BE
Silva; Teresa Cabezon	Lenkebeek				BE
Fernande Delisse; Anne-Marie Eva	Gosselies				BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese				BE
Lombardo-Bencheikh; Angela	Wavre				BE

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1, 435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	A STEPHEN	Claims	KWIC	Draw, De

☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY
Edwards; Stirling John Northcote AU
Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7, 536/23.1, 536/23.72, 536/24.3

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw. De

□ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

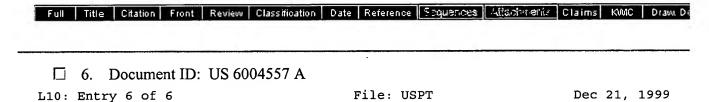
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NAME CITY STATE ZIP CODE COUNTRY

Webb; Elizabeth Ann Eltham AU
Edwards; Stirling John Northcote AU

US-CL-CURRENT: $\underline{424}/\underline{199.1}$; $\underline{424}/\underline{192.1}$, $\underline{435}/\underline{235.1}$, $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{325}$, $\underline{435}/\underline{69.1}$,

<u>435/69.7</u>



US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

DATE-ISSUED: December 21, 1999

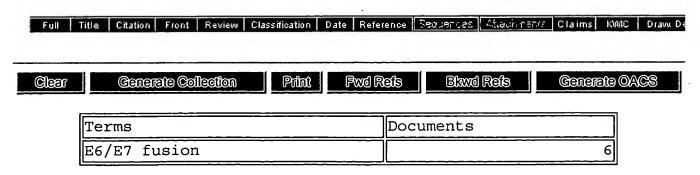
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Edwards; Stirling John Caburg AU
Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia. AU

Flazer; lang St. Bucia.

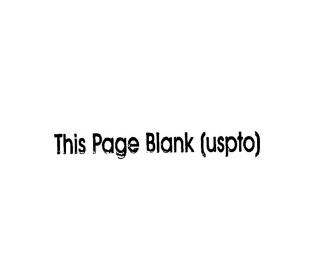
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L2	E6/E7 fuion	0
L1	Zhou xiaoshan.in.	0
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END OF SEARCH HISTORY

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Adw15636 Amti-al
Ace40816 Anti-al
Ace40817 HPV 16
Ace58871 HPV 16
Ace133078 HPV16
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The present sequence represents a fusion protein, comprising E7 and E6 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E7E6PentM, and comprises an E7 amino terminus CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6 CC (arboxy terminus (where residues 63 and 106 have been replaced with G1ycine). E7E6PentM is representative of fusion proteins of the CC glycine). E7E6PentM is representative of fusion proteins of the E7 polypeptides, where the E7 polypeptide has mutations at any one or more CC of the amino acids corresponding to amino acids 24, 26 or 91 of the Sequence given in ADO44073 and the E6 polypeptide has no mutations or has CC mutations at any one or more of the amino acids corresponding to amino CC acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus CC immune responses against HPV. They are also useful for treating lower gastrointesting tract cancers, e.g. and cancer, and other cancers of the animosetical cancer also useful for treating lower gastrointesting tract cancers, e.g. anal cancer, and other cancers of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16. Synthetic.
                                                              Sequence 248
                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-316328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer;
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                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel vaccine composed of an antigen protein and a second protein as an s-(methyl mercury)-1-cysteine (CMH class II) ligand. The second protein is taken from a group including human Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures. The viral antigens can be for hepaticis B (HBV), human papillomavirus (HBV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-Barr virus (EBV), cytomegalovirus (CWV), and their combinations. The bacterial antigens can be intracellular bacteria of tuberculosis, leprosy and listeria. A vaccine of the invention has virucide, and antibacterial
                                                                                                                                                                                                                                                                                                                                                                     Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Therapeutic vaccine, for viral and bacterial conditions, comprises antigen protein and a viral or bacterial protein, coupled together stable hydrogen or covalence bonds in biological media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-678227/70.
N-PSDB; AED13077.
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                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity. The present sequence represents the HPV16 variant E7 protein
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    French.
                                                                                                                                                                                                                                     Score 513; DB 9; Lo
Pred. No. 1.6e-57;
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                                                                                                                                                                                                                                                                                                     Length 98
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                                                                                                                                                                                                                                               Gape
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RESULT 4
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-405485/34.
N-PSDB; AAX78794.
                       Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy; tumour; lesion; benign; malignant; virus; infection.
                                                                                                                                              17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                         AAY02634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein;
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                                                                                                                                                                                                                                                                    AAY02634 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                             Prot.D1/3-E7-mut(C24G,E26Q)/HPV16 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
logical fusion partner; CpG oligonucleotide; immune response;
tigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 513; DB 2;
Pred. No. 4.6e-57;
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RESULT 5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus.
Haemophilus influenza
Chimeric.
                                                                                          Haemophilus influenzae; strain
Human papillomavirus type 16.
Synthetic.
                       Misc-difference
                                                                                                                                                                                                          29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1999
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                                               Misc-difference
                                                                                                                                                         Fusion
                                                                                                                                                                                Fusion protein D1/3-E7-His(HPV16), C137G/E139Q
                                                                                                                                                                                                                                                         AED52640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                            protein; vaccine; papilloma;
de; uterine cervix tumor; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX29783
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                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AA;
                                                                                                                                                                                                                                                      standard; protein;
                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                       /note= "Wild-type Cys substituted by Gly" 139
                                              Location/Qualifiers
           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                               96.9%;
          "Wild-type Glu substituted
                                                                                                                                                                                                                                                         220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 513; DB 2;
Pred. No. 4.6e-57;
0; Mismatches 3
                                                                                                                                            cytostatic; papillomavirus infection; mutein; D protein.
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RESULT 6
AD044068
ID AD04
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyta protein (CLyta) or thioredoxin. The present sequence represents a mutated HPV-H. influenzae D protein, fusion protein of the invention.
                                                                                                                                                                                                       E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer anal cancer; reproductive system cancer; penile cancer; vulvar cancer
                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-2005.
 Smith L,
                                                      03-OCT-2002; 2002US-0415929P
                                                                                02-OCT-2003; 2003WO-US031726
                                                                                                             15-APR-2004.
                                                                                                                                                                             Human papillomavirus type 16.
                                                                                                                                                                                                                                                               Amino acid sequence of a fusion
                                                                                                                                                                                                                                                                                                                    ADO44068;
                                                                                                                                                                                                                                                                                                                                              ADO44068 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 220 AA;
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                            (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                       WO2004030636-A2
                                                                                                                                                                                                                                                                                          15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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 Cassetti MC
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                                                                                                                                                                                                                                                                                          (first entry)
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96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 513; DB 9;
Pred. No. 4.6e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                         CC The present sequence represents a fusion protein, comprising E7 and E6 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E7E6TEHM, and comprises an E7 amino terminus (where CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy CC terminus (where residues 63 and 106 have been replaced with glycine). CC S7E6TEHM is representative of fusion proteins of the invention. The CC where the E7 polypeptide human papillomavirus E6 and E7 polypeptides, CC where the E7 polypeptide has mutations at any one or more of the amino CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any core or more of the amino acids corresponding to amino acids 63 or 106 of CC there sequence given in ADO44072. The polypeptides of the invention are CC useful for treating or preventing human papillomavirus (HPV)-associated CC cancers, such as cervical cancer. The fusion proteins and nucleic acids CC cancers fusion proteins are useful for generating immune responses CC against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive insured including papillomavirus cancers.
                                                                                                                                                                                    Matches
                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                         Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                    system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 73-74; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADO44069.
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                                                                                                                                                                                                       Local
                                             61
61
                                                                                                                                       -
                                                                                                                                                                                    95;
                                                                                                                                                                                                       Similarity
                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                          MHGDTPTLHEYMLDLQPETTDLYGYGQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                    96.9%;
                                                                                                                                                                               Score 513; DB 8; I
Pred. No. 5.3e-57;
0; Mismatches 3;
                                                                                                                                                                                                                          Length 248;
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RESULT 7

ADA27366
ID ADA2
XX ADA2
XX ADA2
XX ADA2
XX COLI
XW Cell
XW Dacu
XW Giac
XW Fusi
XX W MO20
XW WO20
XW MO21
XW ADA2
XX ADA2
X
                                            14-FEB-2002;
14-FEB-2002;
14-FEB-2002;
14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell line; American Type Culture Collection PTA-4047; ATCC-4047; baculoviruses; viral recombinant protein; virus-like particle; vacc diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                 2002US-0356118P.
2002US-0356119P.
2002US-0356123P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002; 2002US-0356133P.
14-FEB-2002; 2002US-0356135P.
14-FEB-2002; 2002US-0356151P.
14-FEB-2002; 2002US-0356151P.
14-FEB-2002; 2002US-0356152P.
14-FEB-2002; 2002US-0356154P.
14-FEB-2002; 2002US-0356156P.
14-FEB-2002; 2002US-0356167P.
14-FEB-2002; 2002US-0356162P.
14-FEB-2002; 2002US-0356162P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a cell line comprising a cell that is a clone, derivative, mutant and/or transfectant of a cell line designated American Type Culture Collection (ATCC) PTA-4047. The cell upon culture grows continuously and retains the identifying characteristics of the cell line designated ATCC-4047. Also described is a process of making a cell line. The insect cell line sussful in replicating baculoviruses, as a host substrate for baculovirus plaque assays, as a source of insect proteins, acts as depot for cell transfection to produce recombinant baculoviruses, and in expressing viral recombinant proteins. Extracellular and intracellular viral recombinant proteins and virus-like particles expressed from the cell line are useful as pharmaceutical compositions, vaccines or diagnostic reagents. The present sequence represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion protein, which is used in the exemplification of the present invention.
                                                                                            codon optimised; viral capsid protein; virus-like particle; VLP;
antigenic; human papillomavirus infection; virucide; vaccine;
gene therapy; human papillomavirus type 16; dysplasia; infection
                                                                                                                                                               HPV-16 L2/E7/E2 fusion
                                                                                                                                                                                                                                                               ADA92544 standard; protein; 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 59-60; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          baculoviruses to produce large amounts of recombin medical, pharmaceutical and veterinary importance.
                                                                                                                                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New insect cell line designated ATCC PTA-4047, useful for replicating
                            Human papillomavirus type 16
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DB; ADA27374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQASPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805
                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 568
                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYGYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.2%;
96.9%;
                                                                                                                                                               amino
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Pred. No. 2.4e-56;
                                                                                                                                                             acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                               SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 805;
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                                                                                                                                                                 9:0N
                                                                                            infection; HPV-16;
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WO2003068933-A2

Query Match

99.2%;

Score 513;

명 7;

Length 805;

Sequence

805 AA;

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The present invention describes a codon optimised polynucleotide encoding CC a viral capsid protein that self assemblee into a virus-like particle CC (VLP) that exhibits conformational antigenic epitopes capable of raising CC neutralising antibodies, where the VLP is expressed from a host cell comprising that a particle extracellularly. Also described: (1) a vector comprising the above codon coptimised polynucleotide operably liked to a eukaryotic or prokaryotic coption control element, capable of replication in prokaryotic and/or ce eukaryotic host; (2) a host cell comprising the vector; (3) a control element, capable of replication in prokaryotic and/or ce pharmaceutical or vaccine composition for treating, ameliorating or comparation and integration, comprising and thisplicity of VLPs that exhibit conformational antigenic epitopes, and ce acarrier, diluent or adjuvant; (4) a diagnostic kit for detecting a papillomavirus infection, comprising a multiplicity of VLPs that exhibit conformational antigenic epitopes, and cetection agent comprising a conformational antigenic epitopes, and a detection agent comprising a conformational antigenic epitopes, and a detection agent comprising a colons that are utilised at high levels in insect cells with codons that are utilised at high levels in insect cells with codons that are utilised at high levels in insect cells with codons that are utilised at high levels in insect cells in titally-modified sequence by choosing a preferred codon contitially-modified sequence by choosing a preferred codon cells towards about 1:1, where the ratio of GC nucleotide sequence creates towards about 1:1, where the number of palindromic and steen-loop pairs to AT nucleotide pairs in the further-modified nucleotide sequence is minimised, and (6) methods for treating, ameliorating or created above. The VLP has virucide activity and can be used in vaccines can sequence is minimised, and (6) methods for the present invention conformation and methods of the present invention can feet and the pr
14 FEB 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New codon optimized polynucleotide encoding a viral capsid protein that self assembles into a virus-like particle, useful for diagnosing, preventing or treating human papillomavirus infections or associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2003;
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2002US-0356150P.
2002US-0356151P.
2002US-0356151P.
2002US-0356154P.
2002US-0356154P.
2002US-0356156P.
2002US-0356167P.
2002US-0356167P.
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2002US-0356123P.
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ADA14293
ADA
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14-FEB-2002;
14-FEB-2002;
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14-FEB-2002;
14-FEB-2002;
The present invention describes a method for purifying a recombinant extracellular or intracellular virus-like particle (VLP). The method comprises harvesting a cell suspension comprising cells containing a plurality of VLPs to produce a harvested supernatant, optionally disrupting the harvested cells to produce cell lysates containing the VLP, clarifying the harvested supernatant, concentrating the clarifies supernatant, disfiltering the concentrated supernatant, and recovering the purified recombinant VLP. Also described: (1) a cell line designates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purification; recombinant extracellular virus-like particle; recombinant intracellular virus-like particle; HPV; infection; dysplasia; HPV-16; fusion protein.
                                                                                                                                                                                                                                                                                              Purifying a recombinant human papillomavirus (HPV) L1, useful for diagnosing, preventing or treating HPV infections, comprises clarifying, concentrating and diafiltering cells containing HPV particles.
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                                                                                                                                                                                                                                                   Disclosure;
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14-FEB-2002;
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2002US-0356129P.
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2002US-0356133P.
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2002US-0356151P.
2002US-0356154P.
2002US-0356154P.
2002US-0356154P.
2002US-0356156P.
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2002US-0356161P
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                                                                                                                                                                                                                                                   English.
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                               concentrating the clarified supernatant, and recovering
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RESULT 10

AAE38618

ID AAE38

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Best Local
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                                                                                                                                                                                                                                           14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 805 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; humoral immunity; cell-mediated immunity; gene therapy; virucide; papillomavirus infection; Human papillomavirus; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPV-16 L2/E7/E2 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE38618 standard; protein;
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                                                     Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2003; 2003WO-US004473.
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                                                                                                           NOVAVAX INC.
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2002US-0356123P
2002US-0356129P
2002US-0356139P
2002US-0356139P
2002US-0356139P
2002US-0356151P
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2002US-0356157P.
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2002US-0356154P.
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Pred. No. 2.4e-56;
0; Mismatches 3
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to chimeric virus-like particle comprising a recombinant viral capsid protein that encapsulates a recombinant viral protein during self assembly into a chimeric virus-like particle and exhibiting conformational antigenic epitopes capable of eliciting neutralising antibodies. The vaccine comprising the chimeric virus-like particles are useful for inducing immunity (humoral and/or cell-mediated immunity) against papillomavirus infection. The invention is also useful in gene therapy. The present sequence is HPV (human papillomavirus)-16
The peptide is the sequence of the human papillomavirus HPV 16 E7 nucleoprotein. Peptides corresponding to regions (pref. epitopic regions of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these
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21-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 122-123;
                                                                                                                                                                                                                                                     26-SEP-1990;
                                                                                                                                                                                                                                                                                   26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV E7 peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 805
                                                                                                                    Immunogenic peptide(s) derived from E6 or E7 region of HPV16 recombinant cells encoding them, useful in treatment and pro
                                                                                                                                                                WPI; 1992-132119/16.
                                                                                                                                                                                                                                                                                                              02-APR-1992.
                                                                                                                                                                                                                                                                                                                                           WO9205248-A.
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                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric virus-like particles comprising a recombinant viral capsid tein encapsulating a recombinant viral protein, useful for inducing oral and/or cell-mediated immunity against papillomavirus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                       warts
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                                                                         Fig 7; 81pp;
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(first entry)
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                                                                                                         cancer
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                                                                                                                                                                                           Blake J,
                                                                         English.
                                                                                                    resulting
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Pred. No. 2.4e-56;
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                                                                                                                                                                                             Hellstrom
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prophylaxis
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ARESULT 12
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                                                                                                                                                                                           Sequence 98 AA;
                                                                                                                                                                                                                                    The sequence is that of the human papillomavirus type 16 E7 protein. protein sequence was aligned with that of bovine papillomavirus type See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                         Use of papilloma-virus E7 protein or fragments for the therapy of papilloma-virus disease - for the regression of tumours e.g. removal of warts from udders or mouth of milking cows or for treatment of horses o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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21-MAY-1994
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                                                                                                                                                                                                                                                                                                                                         Disclosure;
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95; Conserv
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                                                                                                                         Similarity
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                         MHGDTFTLHEYMLDLQPETTDLYXYXQLNDSSBEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
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MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                    Score 512;
Pred. No. 2.
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                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512; DB 2;
No. 2.2e-57;
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                                                                                                                       DB 2;
.2e-57;
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents Human papillomavirus (HPV), strain 16, E7 oncoprotein. The proliferative state of a cell transformed with HPV can be evaluated in the following manner. Cyclin/cyclin-dependent kinase complexes containing protein p21CIP1 (AAW46807-88) are isolated from the transformed cell, and the HPV E7 oncoprotein added to the isolated protein. Cyclin/cyclin-dependent kinase complexes are isolated from an untransformed cell that is substantially homogenic with the transformed cell, and the HPV E7 oncoprotein added. The kinase activities of the 2 samples are measured, where a proliferating transformed cell has a greater kinase activity that the untransformed cell. The method is used for determining the extent of interaction and/or inactivation between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and thus evaluating the proliferative state of a transformed cell. (Updated thus evaluating the proliferative state of a transformed cell. (Updated the correct of first state of a transformed cell. (Updated the correct of the proliferative state of a transformed cell. (Updated the correct of the correct of the correct of the correct of the cell in the correct of the cell in the correct of the cell in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluation of proliferative state of cells transformed with human papilloma virus - by determining cyclin-dependent kinase activity induced by E7 onco-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E7 oncoprotein; proliferative state; HPV; kinase activity; cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation; cyclin/cyclin-dependent kinase inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYXXYQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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CDSTLRLCVQSTHVDIRTLEDLLMCTLGIVCPICSQKP
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Pred. No. 2.2e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel assay for identifying compounds which ci inhibit viral replication and pathogenesis by increasing proteasomal replication and pathogenesis by increasing proteasomal rection. The method comprises reacting a compound with proteasomal protein (20% proteasomes separately with or without 19% and 11% complexes), viral gene product, and protein or peptide substrates; measuring protease activity; and identifying the compound as an inhibitor if the protease activity of the assay system is increased. The assays of the invention can be used to identify compounds which inhibit viral replication and pathogenesis, and compounds are of value in the treatment of viral compounds which increase proteasomal degradation of viral components or molecules induced by viral infection are of value in the treatment of viral disease. Compounds which inflammatory disease, and AIDS in HIV infected patients. The methods may caffed to proteasomal function to bacterial or viral damage.
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 95; Conserv
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13-JUN-1998;
13-JUN-1998;
13-JUN-1998;
                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel assay methods for identifying
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                                                                                                                                                                                                                                                                                                                                                                proteasomal function
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                         98 AA;
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                                                                                                                                                                                            Conservative
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98GB-00012759.
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98GB-00012757.
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                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                         Score 512; DB Pred. No. 2.2e 0; Mismatches
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                                                                                                                                                                                                                      DB 3;
.2e-57;
                                                                                                                                                                                                                                              Length
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP

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AC CA22
AC ACA22
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RESULT 16
AAB98421
ID AAB98
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genital warts such as condylomata acuminata. However, the type and severity of disease caused by the papillomavirus is dependent on the strain causing the infection. The present sequence represents the human papillomavirus 16 E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a fusion protein comprising 2 amino acids sequences from 2 different papillomavirus specific (PVS) proteins. The fusion protein may be administered for preventing and treating papillomavirus infections in humans and animals. Papillomaviruses are implicated in the pathology of malignant tumour formation in the anogenital tract (of these tumours, cervical cancer is the most frequent (50000 cases/year) and in the formation of precursor lesions of cervical intraepithelial neoplasia (CIN). Papillomaviruses also cause benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pusion proteins comprising papillomavirus specific proteins useful for vaccinating against malignant tumors of the anogenital tract such as cervical carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic; viral capsomere; virucide; dermatological; malignant tumour formation; cervical cancer; cervical intraepithelial neoplasia; genital wart;
                               AAB98421;
                                                                                        AAB98421 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-063092/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condylomata acuminata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus 16 E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY57721 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 34; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDIGENE GMBH.
                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hallek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98CA-02229955.
                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 512; DB 3;
Pred. No. 2.2e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98
                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                   60
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RESULT 17
AAU01718
ID AAU01
XX
AC AAU01

AAU01718 standard; protein; 98 AA

AAU01718;

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                                                                                                                                                                                                                                           The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine (C present invention are useful for stimulating nucleic acid compositions from the C present invention are useful for stimulating an immune response to HPV by c stimulating the production of CTL or HTL responses, specifically in the C manifested symptoms e.g. genital warts or neoplastic growth. The peptides can also be used in a tetramer staining assay to assess peripheral blood c mononuclear cells for the presence of antigen-specific CTLs following c exposure to a pathogen or immunogen, and as reagents to evaluate immune compositions are useful for removing warts or treating HPV infections. The epitopes for inclusion in an epitope-base vaccine may be selected c from conserved regions of viral or tumour-associated antigens, which c reduces the likelihood of escape mutants, also immunosupressive epitopes that may be present in whole antigens can be avoided with the use of c epitope-base vaccines. An additional advantage is the ability to combine c epitopes achieving enhanced immunogenicity, the major benefit of the composition of that is safe and efficacious. AAB98391 to AAB98477 represent convertion.
                                                                                                                                   Matches
                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                  Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 21; 756pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated human papilloma virus (HPV) epitope, useful in vaccines for treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-381497/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart; neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2000; 2000WO-US033549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200141799-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papillomavirus protein HPV16
61
                              61
                                                                                                                                   95;
                                                                                                                                                   Similarity
                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sidney J,
                                                                                                                                                                                                    Ą,
                                                                                                                                   Conservative
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                                                                                                                                                   96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood S,
                                                                                                                                 Score 512; DB 4; L
Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celis
                                                                                                                                                                   Length 98;
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grey HM;
                                                                                                                                   <u>,</u>
                                                                                                                                   Gaps
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cc cyropiasmic translocation domain of a pseudomonas exotoxin A (ETA dII), cor a granulocyte-macrophage colony stimulating factor (GM-CSP); and (b) a cc second polypeptide domain containing an antigenic polypeptide. A cc composition comprising the chimeric polypeptide is useful for inducing an immune response such as a cytotoxic T cell response. The nucleic acid or vector encoding the chimeric polypeptide present in the composition is created as naked DNA by gene gun or equivalent, or by liposomal formulation. These are thus useful for vaccinating a mammal against composition is response to a pathogen. Preferably they care useful for vaccinating a mammal against a tumour antigen. The compositions and methods are useful for stimulating or enhancing the created monogenicity of a selected antigen or stimulating or enhancing a cellular immune response specific for that antigen. The chimeric nucleic acid molecules and vaccination methods, yield potent antigen-specific immunotherapy. The polynucleotides and DNA vaccines can induce a cellular immune response that is at least 40 fold more potent than conventional CC domesticated or agricultural animals, as well as humans, and have low cmmunogenicity
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                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the amino acid sequence of human papilloma virus-
16 (HPV-16) E7 antigen used in construction of a chimeric polypeptide
comprising; (a) a first polypeptide domain containing a carboxy terminal
fragment of a heat shock protein (HSP), an Flt-3 ligand (FL), a
cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric polypeptide, useful as anti-tumor vaccines, comprises carboxy terminal fragment of heat shock protein, Flt-3 ligand or cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
                                                                                                                                                                                                                                             Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-290921/30
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09-FEB-2000; 2000US-00501097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF; chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ET antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine; immunotherapy; HPV-16; E7 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 39; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS02608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000; 2000WO-US041422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus-16 (HPV-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2001 (first entry)
                                      61
                                                                                                                                                              95;
                                                                                                                                                                                 Similarity
                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQABPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                              Conservative
                                                                                                                                                                                 96.9%;
                                                                                                                                                         Score 512; DB 4; Length 98; Pred. No. 2.2e-57; O; Mismatches 3; Indels
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                                                                                                                                                            <u>,</u>
                                                                                                                                                            Gaps
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1 MHGDTPTLHEYMLDLQPETTDLXXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

Indels

٥,

Gaps

60

Matches Query Match

Local Similarity

Conservative

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RESULT 18
AAU72607
ID AAU72
                                                                             CC dependent kinase-2 (CDK2) kinase (I) activity, comprising measuring (I) CC dependent kinase-2 (CDK2) kinase (I) activity, comprising measuring (I) CC activity on CDK2 substrate in the presence of human papillomavirus (HPV) CC E7 or its fragment, and in the presence and absence of test compound. The case of compound is identified as inhibitor of E7-induced (I) activity when CC decreased phosphorylation of CDK2 substrate is detected. The method is CC used for identifying inhibitor of E7-induced CDK2 kinase activity. This CC identifying an inhibitor of E7-induced increase in CDK2 kinase activity. This CC measuring viral proliferation in the presence and absence of identified cC inhibitor and identifying the inhibitor as an antiviral agent when CC decreased proliferation is detected, in the presence of the inhibitor. The CC compared to viral proliferation in the absence of the inhibitor. The CC dentified inhibitors are useful for reducing HPV E7-induced kinase activity or for ameliorating HPV proliferation by inhibiting E7-induced contivity or for ameliorating HPV proliferation by inhibiting E7-induced contivity or for inhibitors identified by the above method are useful for produced medicament for ameliorating viral infection e.g. HPV CC infection, adenoviral infection or similar virus 40 (SV40) infection. The CC correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying E7-induced cyclin-dependent kinase-2 activity inhibitor, comprises identifying test compounds which reduce cyclin-dependent kina-2 substrate phosphorylation in presence of human papillomavirus E7 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus; HPV; E7; cyclin E; cyclin A; virucide; E7-induced cyclin-dependent kinase-2; CDK2 kinase; HPV infecadenoviral infection; simian virus 40 infection; SV40.
                                                                           Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2003
26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 12-13; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1999; 99US-00382616.
25-AUG-2000; 2000US-00648215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000; 2000US-00728466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2001029022-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus (HPV) E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU72607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU72607 standard; protein; 98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FISH/) FISHER C.
(HEWW/) HE W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                 99.0%;
Score 512; DB 4; Li
Pred. No. 2.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPV infection;
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RESULT 19
AAB67546
ID AAB67
XX E7-in
XX E7-in
XX Viral
XX Viral
XX Viral
XX VIral
XX VIRA
XX E7-AL
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PR 25-AL
XX VIRA

RESULT 20
AAB86332
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                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a method for identifying inhibitors of E7-induced CDK2 kinase activity. The method comprises measuring CDK2 kinase activity on a CDK2 substrate in presence of human papillomavirus (HPV) E7 (or fragment), in presence and absence of a test compound and measuring phosphorylation of substrate. The method is useful for identifying an inhibitor of E7-induced CDK2 kinase activity. The identified inhibitor is useful for reducing or inhibiting HPV proliferation in an individual. Inhibitors of E7 binding to the CDK2 complex are useful in preparing medicament for ameliorating viral infection e.g. HPV infection, adenoviral or SV40 infection. The present sequence represents a papillomavirus E7 fragment, which is used in the method of the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying inhibitors of human papilloma virus E7 protein-induced increase in CDK2 kinase activity for use as antiviral agent, by mekinase activity on CDK2 substrate in presence of E7 protein, test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-2003
29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 40; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                               Score 512; DB 4;
Pred. No. 2.2e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for immunizing an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and its encoding DNA (I) for immunizing an individual against diseases, in particular against infection-induced auto-immune and tumor diseases. This sequence represents a fragment of the human papillomavirus E7 protein used in the preparation of the fusion constructs described in the method
 Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide; cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA venhanced antigen-specific immune response; cytotoxic T lymphocy tumour; cancer; cervical cancer.
                                                                      Human papillomavirus 16 (HPV16), E7
                                                                                                   05-JUN-2002
                                                                                                                                                        AAU77713
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 23pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; VP22; E7; cell import signal; cell export signal; antigen; immunization; infection-induced auto-immune disease; tumor disease.
                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying inhibitors and activators of eukaryotic potassium channels, for use as therapeutic agents, comprises using a transformed yeast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2001; 2001WO-DE000134.
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                                                                                                                                                      standard; protein;
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                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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Pred. No. 2.2e-57;
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                lymphocyte;
                             DNA vaccine;
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RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide comprising a first polypeptide domain comprising and a second polypeptide domain comprising at least one antigenic peptide e.g. altreticulin (CRT) and a second polypeptide domain comprising at least one antigenic peptide e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune responses, particularly those mediated by cytotoxic T lymphocytes. The nucleic acid and compositions comprising the nucleic acid is also useful for inhibiting the growth of tumours and cancers e.g. cervical cancer. This is the amino acid sequence of the human papillomavirus type 16 (HPV 16) early gene 7 (E7) used in the creation of a DNA vaccine
                                                                                                                        Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma; adenocarcinoma; koilocytosis; hyperkerotosis; intraepithelial neo; intraepithelial lesion; dysplasia; head cancer; neck cancer; small cell lung cancer; melanoma; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding a fusion polypeptide comprising an endoplasmic reticulum chaperone polypeptide linked to an antigenic polypeptide, useful as a vaccine for inducing antigen-specific immune responses.
                                                             Key
                                                                                                                                                                                                                                          29-AUG-2003
14-FEB-2002
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                                                                                            Human papillomavirus type 16.
                                                                                                                                                                                                        Human papillomavirus (HPV) 16, E7 coding region.
                                                                                                                                                                                                                                                                                         AAU10810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 32; 71pp; English
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                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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(first entry)
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/label= E7 peptide_epitope_1
/note= "This region is specifically referred to in claim
2"
                                                          Location/Qualifiers
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Pred. No. 2.2e-57;
0; Mismatches 3
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08-JAN-2003

(first entry)

ABB82375

standard;

protein;

98

ABB82375;

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RESULT 23
ABB82375
ID ABB82
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AC ABB82
XX
DT 08-JA
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 AA;
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es 95; Conserv
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                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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/label= E7 peptide_epitope_2
/note= "This region is specifically referred to 2"
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RESULT 24
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ID AAO16
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AC AAO16
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DT 15-M2
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DT 15-M2
XX
KW Epitc
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypeptide, comprising a first nucleic acid sequence encoding a polypeptide, optionally, fused in frame with the nucleic acid, a linker polypeptide optionally, fused in frame with the nucleic acid, a linker concleic acid encoding a linker peptide, and a nucleic acid that is linked in frame to them, and that encodes an antigenic peptide or polypeptide. CC The nucleic acid molecule, polypeptides and vectors are useful as concleic acid molecule, polypeptides and vectors are useful as concleic for enhancing immune responses, primarily cytotoxic contingens for inhibiting growth or preventing re-growth of a tumour. CC lymphocytes (CTL) responses to specific antigens such as tumour or viral contingens, and for inhibiting growth or greventing re-growth of a tumour. CC particles without contamination from replicon-competent virus. The contamination from replicon-competent virus. The pathogenic organisms include viruses such as human papilloma virus (HPV), hepatitis B virus, hepatitis C virus, human immunodeficiency virus, bepatitis B virus and herpes simplex virus, intracellular parasites such as malaria, and bacteria that grow intracellular parasites such as malaria, and bacteria that grow intracellularly such as mycobacteria conditions.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding an antigenic fusion polypeptide useful as vaccines for enhancing or inducing immune responses, primarily cytotoxic T lymphocytes (CTL) responses to specific antigens such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid molecule that encodes a fusion polypeptide, comprising a first nucleic acid sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 19;
                                 Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-740856/80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2001; 2001US-0276854P
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Epitope; 87
                                                                                                        AA016630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-2002; 2002WO-US008033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type HPV-E7 protein sequence
                                                                     15-MAY-2003
                                                                                                                                        AAO16630 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or viral antigens.
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                                                                                                                                                                                                                                                                                                  95;
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                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                          Conservative
antigen; CD4-positive T cell activation;
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y; cytostatic; virucide; protozoacide; antibacterial; CTL;
anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;
                                                                                                                                                                                                                                                                                                                                                                                         99.0%;
                                 E7 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93pp; English.
                                                                                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                       Score 512; DB 5;
Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                98
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RESULT 25
ADF09516
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises an epitope of the human papillomavirus E7 ant that is capable of activating CD4-positive T cells that are specific uterine cancer lesions. The epitope of the invention is useful for preventing and treating uterine cancer. The present amino acid sequen represents the human papillomavirus E7 antigen
                                                                                                                                                                                                                                                                                  ADF09516 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel epitope of human papilloma virus E7 antigen capable of activating CD4-positive T cells specific to (pre-)uterine cancer lesion, applicable in drug compositions for preventing and treating uterine cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-156946/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-2001; 2001JP-00173803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uterine cancer lesion
         Jackson
                                                                                                                                                                                                                                       12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 34; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maeda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-2002; 2002WO-JP005747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16
                                                                                                              21-AUG-2003
                                                                                                                                  WO2003068940-A2
                                                                                                                                                         Human papillomavirus
                                                                                                                                                                              human papilloma virus; HPV; cancer.
                                                                                                                                                                                                                Human papillomavirus 16 E7 SEQ ID NO:17.
                                (CURA-) CURAGEN CORP.

(HOFF) HOFFMANN LA ROCHE INC.
                                                                14-FEB-2002; 2002US-0356911P
                                                                                       14-FEB-2003; 2003WO-US004594
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                         protein-protein interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okubo M;
          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
         Lewin DA,
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Pred. No. 2.2e-57;
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           Cuthill
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                           virucide;
                                                                                                                                                                                           cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequence
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RESULT 26
ADF18632
ID ADF18
XX ADF18
AC ADF18
XX ADF18
XX HPV;
XX HPV;
XX HPV;
XX HUMAN
XX HO20(
XX HUMAN
XX HOZO(
XX WPI;
DA (UYR)
XX WPI;
DA N-PS;
XX D18c
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Best Local Similarity
Matches 95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel purified complex comprising a first polypeptide and a second polypeptide, where the polypeptides comprise defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytostatic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing a conditions involving altered level of the complex, e.g. human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases. The sequences shown in ADF09500-ADF09583 represent proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified complex comprising a first polypeptide and a second polypeptide, useful for identifying agents for treating/preventing a condition involving altered level of the complex e.g. human papilloma virus infection, or cancer.
                                                                              Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                          19-APR-2002; 2002US-0374245P
                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV; oncoprotein E7; cytostatic; gene therapy; kinase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                    (UYRP )
                                                                                                                                                                                                                                                                                                                                                21-APR-2003; 2003WO-US012667
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003088922-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF18632 standard; protein;
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DB; ADF09608.
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                                                                                                                                                            ADF18633, ADF18634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                            Westbrook TF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oncoprotein.
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Disclosure;

SEQ ID

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8,

119pp; English

present

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RESULT 27
ADL90076
ID ADL90076
AC ADL90
XX ADL90
XX ITMMU
XX ITMMU
XX ITMMU
XX ITMMU
XX ITMMU
XX ITMMU
XX ITMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                             The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in
                                                                                                                                                                                                                                                                               Generating an immune response to an antigen, useful desired T cell responses comprises administering an one peptide epitope of the antigen attached to the i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
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14-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus 16-E7 protein, SEQ ID 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL90076 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR-) ASTRAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            госат
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95; Conserv
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                                                                                                                                                                                                              Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-0412219P
2003WO-US007995
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                                                                                                                                                                                                                  1G; 154pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith
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Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                                                            ul for generating an immunoglobulin e immunoglobulin.
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                                                                                                                                                                  The specification describes a method for constructing a synthetic polynucleotide from which a polypeptide is producible at a different level in a Chinese Hamster Ovary (CHO) cell compared to when using a parent polynucleotide encoding the same polypeptide. The method comprises selecting a first codon of the parent polynucleotide for replacement with a synonymous codon, where the synonymous codon is selected on the basis that it exhibits a different translational efficiency in the CHO cell than the first codon in a comparison of translational efficiencies of codons in test CHO cells. The method is useful for constructing synthetic polynucleotides which are translated more efficiently, compared to the parent polynucleotide. The present sequence represents Human papillomavirus type 16 (HPV16) E7 protein. The E7 polynucleotide was codon-modified, to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constructing a synthetic polynucleotide, useful for producing a polypeptide at a higher level in a Chinese Hamster Ovary cell, compriselecting a first codon of the parent polynucleotide for replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-270043/25.
N-PSDB; ADM32915, ADM32917.
                                                                                                                Sequence 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM32916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004024915-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of HPV16 E7 protein.
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                            Score 512; DB 8; Length 98; Pred. No. 2.2e-57;
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Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a wild type E7 protein from human papillomavirus type 16 (HPVI6), which is used to produce fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV) -associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 16. Synthetic.
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                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 77; 101pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to papilloma-virus specific (PVS) protein and fusion protein constructs. The invention also relates to vaccine formulations comprising viral capsomeres and methods for their production. The fusion protein is useful for treating or preventing a papilloma virus infection in an animal, particularly humans and is also useful in the production of vaccines. The present sequence is human papilloma virus (HPV) strain HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion proteins comprising an amino acid sequence from a first and a second papilloma-virus specific protein, useful in vaccines for treating or preventing a papilloma virus infection in an animal, particularly
Human papillomavirus type 16
                                          10-FEB-2005
                                                                                                                  ADU66362 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hallek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1998;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papilloma virus (HPV) strain HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
                                                                                ADU66362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIGENE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004081661-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papilloma-virus specific protein; PVS; vaccine; infection; human papilloma virus; HPV; E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN49005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN49005 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                          95;
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                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP
                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                          (first entry)
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99US-00284017.
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                                                                                                                                                                                                                                                                                                                                                                      Score 512; DB 8;
Pred. No. 2.2e-57;
0; Mismatches 3
    (HPV16)
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RESULT 32
ADX15532
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Best Local :
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                                                                                  Human papillomavirus
                                                                                                                                                                                                                                21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccine for inducing or enhancing immune response or for inhibiting or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; MHC class I pathway; antigen specific immune response; tumor;
E7 protein; E6 protein.
                                                                                                                                  High throughput screening; pharmaceutical; antiviral.
                                                                                                                                                                             Human papillomavirus E7
                                                                                                                                                                                                                                                                                                                          ADX15532 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor growth.
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10-FEB-2005.
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95; Conserv
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                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                       protein;
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Pred. No. 2.2e
0; Mismatches
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                                                                                                                                                                                SEQ ID NO:
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2.2e-57;
nes 3;
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08-SEP-2003; 2003US-00657399

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method of ameliorating human papilloma virus (HPV) proliferation. The method involves administering an inhibitor of E7-induced cyclin-dependent kinases (CDK2) phosphorylation or an inhibitor of E7-binding CDK2 kinase complex that reduces HPV E7-induced CDK2 kinase activity. The present sequence is the human papillomavirus E7
                                                                                                                                                                                                                                                                Cytostatic; immunohistol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameliorating human papillomavirus proliferation involves administering inhibitor of E7-induced cyclin-dependent kinases 2 phosphorylation or inhibitor of E7-binding cyclin-dependent kinases 2 kinase complex that reduces kinase activity.
New combination of antibodies comprises an anti-HPV-16 E7 antibody and anti-HPV-18 E7 antibody, useful for preparing a diagnostic composition
                                                                                                                                                                                           WO2005026731-A1
                                                                                                                                                                                                                                                    anogenital;
                                                                                                                                                                                                                                                                                                     HPV 16
                                                                                                                                                                                                                                                                                                                            02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                          ADY69083 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-1999; 99US-00382616.
01-DEC-2000; 2000US-00728466.
                                                                     Zwerschke WP,
                                                                                                                                           17-SEP-2004; 2004WO-EP010484.
                                                                                                                                                                                                                Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                   ADY69083;
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                                                                                              (AMYN-) AMYNON
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(HEWW/) HE W.
                                    2005-242459/25
DB; ADY69082.
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                                                                                                                                                                                                                                                  Gene Therapy; human papillomavirus; E7 protein; logical detection; Pap-smear; cervical; carcinoma; mamma; head; neck; prostate; sexually transmitted
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                                                                                                                     2003EP-00020564.
                                                                                                                                                                                                                                                                                                                            (first
                                                                     Jansen-Duerr
                                                                                              BIOTECH GMBH.
                                                                                                                                                                                                                                                                                                                                                                          protein;
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Pred. No. 2.
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                                                                     Fiedler M,
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                                                                                                                                                                                                                                                      disease;
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Best Query Match

Local

Sequence 98

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Length 98;

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This sequence represents human papillomavirus-16 (HPV-16) E7 protein. An CC antibody raised against this protein may be used in a combination of cantibodies which comprises an anti-HPV-16 E7 antibody obtainable by CC eliciting an in vivo humoral response against HPV-16 E7 protein or its cfragment in a goat, and affinity-purifying antibodies as obtained in the CC eliciting step, and an anti-HPV-18 E7 antibody. The combination of antibodies is useful for the preparation of a diagnostic composition for the (immuno-) histological detection of high risk HPV E7 protein. The CC (immuno-) histological detection is carried out on Pap-emears, cervical (Carcinoma) biopsies, anogenital biopsies, mamma biopsies, head- or neck biopsies, or prostate biopsies. The diagnostic composition is used for cancer, for measuring the status of an existing sexually transmitted disease or cancer, or for screening therapy efficiency in the treatment CC disease or cancer, or for screening therapy efficiency in the treatment CC disease is a high risk HPV infection or where the cancer is cervical cancer, breast cancer/mamma cancer, prostate cancer, head and neck cancer, breast cancer, and/or anogenital cancer/meoplasia (AIN). The
                                                           combination of antibodies or the diagnostic composition are useful in an in vitro method for the detection of high risk HPV 27 protein. The antibody is useful for detecting E7 protein of HPV-31, HPV-35, HPV-45, HPV-52, HPV-56, HPV-58, and/or HPV-59. It is also useful for the preparation of a diagnostic composition for detecting E7 protein of HPV-16, HPV-18, HPV-31, HPV-33, HPV-35, HPV-45, HPV-52, HPV-56, HPV-58, and/or HPV-59.
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95; Conserv
                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                              99.0%;
nilarity 96.9%;
Conservative
                                                                                                 0,
                                                                                              Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3
98
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RESULT 34
AEA40816
ID AEA40
XX AEA40
AC AEA40
XX 28-JU
DT 28-JU
XX inmur
KW vacci
XX vacci
XX VOCCI
XX VOCCI
XX INMUR
XX
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18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity;
vaccine; immune
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                                                                                                 (UYJO ) UNIV JOHNS HOPKINS
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    Hung
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         Ki:n
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T-cell;

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AEBILT 35
AEBIL1999
ID AEBIL
XX AEBIL
XX AEBIL
XX O8-SE
XX Tumor
XW Tumor
XW Cance
XX Tuman
XX WO200
XX O7-JU
PP 24-DE
XX 24-DE
XX 24-DE
XX (UYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc acid vector comprising a first sequence encoding an antigenic polypeptide cor peptide, and optionally, a second sequence linked to the first cor sequence and encoding an immunogenicity-potentiating polypeptide (IPP); cc and a second nucleic acid vector encoding an anti-apoptotic polypeptide. cc when the second vector is administered with the first vector to a cc subject, a T cell mediated immune response to the antigenic polypeptide. cor peptide is induced that is greater in magnitude and/or duration than cc an immune response induced by administration of the first vector alone. cc minimum ersponse induced by administration of the first vector alone. cc witable for introduction into a cell or an animal by particle composition; a pharmaceutical composition capable of inducing or composition; a pharmaceutical composition capable of inducing or capable of inducing an antigen specific immune response, comprising the particle commune response in a subject; increasing the numbers of CD8+CTLS and a carrier or an excipient; inducing or enhancing an antigen specific commune response in a subject. The nucleic acid composition is useful as an immunogen for inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as cc an immunogen for inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as cc yetostatic acitivity. This sequence represents ananti-apoptotic vector HPV cc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid composition comprising a first nucleic acid vector encoding an antigenic polypeptide and a second nucleic acid vector encoding an anti-apoptotic polypeptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                                                                Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplasm;
cancer; HPV16 E7.
                                                                                                                                                                                                                                                                                      HPV16 E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-367009/37.
GENBANK; NC_001526.
                                                                          24-DEC-2003; 2003WO-NL000929
                                                                                                                                                      WO2005060993-A1
                                                                                                                                                                                          Human papillomavirus
                                                                                                                                                                                                                                                                                                                              08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                    AEB11989
                                                                                                                                                                                                                                                                                                                                                                                                      AEB11989 standard; protein;
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    (UYLE-)
                                      24-DEC-2003; 2003WO-NL000929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 6; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
    VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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    LEIDEN
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    MEDICAL CENT
                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3
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The invention relates to a method of producing a synthetic protein CC comprising an amino acid sequence that is at least 80% identical to a CC naturally occurring antigenic protein of a pathogen or tumor comprising CC chemically synthesizing two or more fragments, chemically ligating the C-CC produce the synthetic protein or its part and optionally repeating the CC second step to sequentially ligate a further neighboring fragment to CC composition of the second step. The invention also relates to a CC composition comprising the protein and a method for treating or CC to the subject the protein or composition in a therapeutically effective amount. In producing a synthetic protein, the neighboring non-overlapping CC fragments are selected to comprise N-terminal cysteine or glycine cresidues. The naturally occurring protein is an HPV protein, e.g. E2, E6 CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6 CC residues. The reventing or treating HPV associated disease, such as a CC concer. This sequence represents an HPV16 E7 protein used in the method control of the method control of the subject of the subject of the subject of treating or treating HPV associated disease, such as a CC cancer. This sequence represents an HPV16 E7 protein used in the method control of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing a synthetic protein of a pathogen or tumor comprises chemically synthesizing two or more fragments of 2-80 contiguous amino acids of sequence, the sequence of two or more fragments are neighboring and non-
Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesizing two or mon
sequence, the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 1;
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                                                                                            Matches
                                                                                                         Query Match
Best Local
61
                      61
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                                                                                                         Similarity
                                                            MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                            Conservative
                                                                                                       99.0%;
                                                                                            0
                                                                                                         Score 512; DB 9;
Pred. No. 2.2e-57;
                                                                                            Mismatches
                                                                                                                 Length 98
98
                                                                                             Indels
                                                                                            <u>,,</u>
                                                                                            Gaps
                                               60
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RESULT 36
AEC96392
ID AEC96
XX AEC96
XX O1-DE
XX HUMAN
KW HUMAN
KW EPITC
XX EPIT
OS HUMAN
XX O20C
XX HUMAN
XX H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV protein E7 from HPV16.
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31-DEC-2003; 02-JUL-2004;

2003US-0533211P. 2004US-0584652P.

EPIMMUNE INC

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03-JAN-2005; 2005WO-US000077

29-SEP-2005

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AEC98873
AEC98873
ID AEC98
XX AEC98
XX 01-DE
XX 01-DE
XX 04-DE
XX 04-DE
XX 04-DE
XX 05-DE
XX HPV_1
XX Humar
XX 4-DE
XX Humar
XX 14-DE
XX 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.ER1.214, and that CC are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the CC polynucleotide, vector and/or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an CC (comprising the polynucleotide, vector or polypeptide), and making the CC polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the cpitopes in the vaccine protein are disclosed in the tables referred to CC polypeptide is useful in preparing a composition for inducing an immune CC defense against human papillomavirus virus (HPV) and thus providing a CC defense against HPV infection and HPV-related cancers. The present convertion is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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(NEWM/)
(MOTH/)
(BAKE/)
(SOUT/)
(BABE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                          Human papillomavirus type 16
                                                                                Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                   HPV_16 Envelope protein E7.
                                                                                                                                                                                                                              01-DEC-2005
                                                                                                                                                                                                                                                                                       AEC98871
                                                                                                                                                                                                                                                                                                                                          AEC98871 standard; protein; 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHEN/)
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SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
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NEWMAN M J.
MOTHE B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
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Pred. No. 2.2e-57;
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Power SD;
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AED13078 ID AED: XX

AED13078 standard; protein; 98

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RESULT 38

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                                                                                                                                                                                                                                     CC Construction surfaces to the polymerocate comparison papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-spitope construct, a polypeptide comprising an amino acid sequence CC encoded by the polymucleotide, a composition (comprising the CC polymucleotide, vector and/or polypeptide and a carrier), a cell CC (comprising the polymucleotide, vector or polypeptide), inducing an CC immune response against human papillomavirus virus (HPV) and making the CC polymucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the El. E2. E6 and E7 proteins. The CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the CC epitopes in the vaccine protesin are disclosed in the tables referred to CC in the claims of the specification. The polymucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune CC response against human papillomavirus virus (HPV) and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a composition of the vaccine of the composition.
                                                                                                                               Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chesnut Chen Y,
                                                                                                                                                                                              Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-2003; 2003US-0533211P.
02-JUL-2004; 2004US-0584652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Page 350; 518pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a new polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BABE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAKE/)
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HUANG M T
POWER S D.
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BABE L M.
CHEN Y.
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                                                             WHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNOGENETICS
                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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Huang MTF,
                                                                                                                             Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3;
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Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a multi-epitope
                                                                                                                                                            Length 98;
                                                                                                                                 Indels
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RESULT 39
AED64360
ID AED64
XX AED64
XX AED64
XX AED64
XX AED64
XX Vacci
KW Fusio
XX Vacci
KW fusio
XX Human
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel vaccine composed of an antigen protein and a second protein as an s-(methyl mercury)-1-cysteine (CMH class II) ligand. The second protein is taken from a group including human Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures. The viral antigens can be for hepatitis B (HBV), human papillomavirus (HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-Barr virus (BBV), cytomegalovirus (CMV), and their combinations. The bacterial antigens can be intracellular bacteria of tuberculosis, leprosy and listeria. A vaccine of the invention has virucide, and antibacterial activity. The present sequence represents the HPV16 wild-type E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Therapeutic vaccine, for viral and bacterial conditions, comprises antigen protein and a viral or bacterial protein, coupled together stable hydrogen or covalence bonds in biological media.
                          Vaccine; therapeutic; fusion protein; E7.
 Human
                                                                                                  12-JAN-2006
                                                                                                                              AED64360
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98
                                                                    Human papillomavirus type 16 E7 protein.
                                                                                                                                                        AED64360 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 51pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triebel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-APR-2004; 2004FR-00003848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2004; 2004FR-00003848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutagen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV16 E7 wild-type protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2868781-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AED13078;
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DB; AED13076.
papillomavirus
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                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen; virucide;
type 16
                                                                                                                                                                                                                                                                                                                                                           99.0%;
                                         papillomavirus infection; virucide; infection;
                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                           Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial.
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                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                       Length 98;
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RESULT 40
AEE94089
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Best Local :
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03-APR-2001;
04-SEP-2003;
                                                                                                                                                                             Gene expression; therapeutic; immune acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to fusion protein comprising papilloma virus-specific (PVS) protein and their encoding polynucleotides. The invention is useful in preparing a composition for treating and preventing papilloma virus infection in humans. The present sequence the Human papillomavirus type 16 E7 protein.
         Smith LR,
                                                                                                                                                                                                                                      23-FEB-2006
                                                                                                                                                                                                                                                                                   AEE94089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein comprising an amino acid sequence from a first esecond papilloma virus-specific (PVS) protein, useful in preparing composition for treating or preventing papilloma virus infection.
                                                                           06-JUN-2005; 2005WO-US019592
                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2005249745-A1.
                                                     04-JUN-2004; 2004US-0576819P
                                                                                                  15-DEC-2005
                                                                                                                        WO2005118874-A1
                                                                                                                                                                    infection; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AED64359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-2005; 2005US-00179478
                               (AMHP ) WYETH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                          CDSTLRLCVOSTHVDIRTLEDLLMGTLGIVCPICSQKP
         Shahabi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00026896.
2001US-00824017.
2003US-00654129.
                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
                                                                                                                                            type 16.
          Sidhu MK;
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Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                             gtimulation; HIV infection;
E7 protein; anti-HIV; virucide;
                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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sequence is
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2006-047579/05

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RESULT 41
ADQ88451
ID ADQ88
XX ADQ88
XX ADQ88
XX ADQ88
XX ADQ88
XX APV16
XX HPV16
XX HPV17
XX HVMar
XX HVMar
XX AV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing a polynucleotide, useful for enhancing comprises assembling oligonucleotides comprising a modified polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of preparing a polynucleotide that provides enhanced expression of a gene, comprising assembling oligonucleotides comprising surrogate codons to form a modified polynucleotide, comprising a predetermined nucleic acid sequence encoding polynucleotide, comprising a predetermined nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2002; 2002RU-00128131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus; HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV16 E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ88451 standard; protein; 99
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                                                                                                                                                                                                                                                                                                                                 22-OCT-2002; 2002RU-00128131.
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                                                        vaccination
                                                                                                                                                                                                                        Paltsev
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                                                                                                                                                                  2004-446846/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                      protein composition, of tumor diseases in
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Pred. No. 2.2e-57;
0; Mismatches 3
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                                                        anus-genital sphere
                                                                                  useful in immunotherapy
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                                                                                                                                                                                                                        Kiselev
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                                                                                  prophylactic
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Disclosure;

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conjugating the antique

antigen

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ADY92615
ID ADY92625
XX ADY9262
XX ADY92
XX ADY92
XX APTION
XX APTION
XX APTION
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XX IMMUNI
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; monoclonal antibody; antibody production; hybridoma; screening; E7 oncoprotein; immuno-diagnosis; diagnostic; immunoconjugate; immunoassay; radioimmunoassay; enzyme-linked immunosorbent assay; transmissible spongiform encephalopathy; cerebroprotective; cervical intraepithelial neoplasia; cytostatic; immunoglobulin.
The new invention relates to methods and compositions that allow production of antigen specific antibodies to antigens that have traditionally been unable to elicit an adequate and specific immune response. The method comprises producing monoclonal antibodies specito an antigen of low immunogenicity by chemically conjugating the ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 99 AA;
                                                                                                                                                                                                                                                 Producing monoclonal antibodies specific to an antigen of low immunogenicity by immunizing an animal with the chemically conjugated antigen, useful for detecting cervical intraepithelial neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2005
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                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KISE/)
(SVES/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADY92615
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-273121/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kiselev VI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2004; 2004WO-RU000373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005028510-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KISELEV V I.
                                                                                                                                                                                                                                                                                                                                                                                   ADY92614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncoprotein protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                           SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                           72pp; English.
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Pred. No. 2.2e-57,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc and a nucleotide sequence encoding HSP70 and transfecting a host cell cwith the plasmid. The nucleotide sequence encoding E7 oncoprotein comprises ADY92614. The nucleotide sequence encoding HSP70 cc comprises ADY92618. Alternatively, the conjugating is performed cc chemically using glucaraldehyde. Screening for specificity is done by cvarious assays such as radioimmunoassay, enzyme-linked immunosorbent cc assay, or sandwich immunoassay. The antibodies are useful for determining cf a subject is at risk of developing spongiform encephalopathy cc comprising an antibody that specifically detects Prion protein. The Prion cc protein peptide comprises ADY92619, ADY92620 or ADY92622. Antibodies specific to E7 oncoprotein are useful for detecting cervical cells and screening the specimen for the presence of E7 oncoprotein. The monoclonal antibodies comprise at least two immunoglobulin isotype is IgG2a or IgG2b. The immunoglobulin isotype has specificity for a different antigenic determinant than the second immunoglobulin isotype. The present sequence HPV16 E7 oncoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                         lymphocyte; E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to a carrier molecule, immunizing an animal with the conjugated antigen, harvesting B cells from the animal, creating a hybridoma from the harvested B cells, and screening the hybridomas for specificity to the native antigen. The antigens can be E7 oncoprotein, Prion protein peptide, hyaluronic acid or matrix metalloprocease 3. The carrier molecule is HSP70. The chemical conjugation comprises creating a plasmid with a nucleotide sequence encoding the antigen, such as E7 oncoprotein
                    N-PSDB; AAF25008
                                      WPI; 2001-138361/14.
                                                                       Siegel M,
                                                                                                                                           08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                        Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB31608 standard; protein; 121
                                                                                                                                                                             10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                   18-JAN-2001.
                                                                                                                                                                                                                                                  WO200104344-A2
                                                                                                                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a His-tagged HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001
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                                                                                                            (STRE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
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                                                                                                          STRESSGEN BIOTECHNOLOGIES CORP.
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                                                                         Chu NR,
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                                                                         Mizzen LA
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Pred. No. 2.2e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 99
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RESULT 44
AAB31616
ID AAB31
XX Heat
XX Iymph
XX Iymph
XX Iymph
XX Iymph
XX Iymph
XX IYMP
PF 10-JU
XX III-JA
XX III-
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                                                                                                                                                                               Screening for compounds that stimulate Th1-like responses in CD4+lymphocyte cells.
                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E7 protein.
                                                                                                                  Example 13; Fig 12; 88pp; English.
                                                                                                                                                                                                                                                                           WPI; 2001-138361/14.
N-PSDB; AAF25023.
                                                                                                                                                                                                                                                                                                                                                                    Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of Hsp10-E7 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB31616 standard; protein; 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (STRE-) STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Госат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                    Chu NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 2.8e-57;
0; Mismatches 3;
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The present sequence represents a fusion protein comprising Mycobacterium tuberculosis heat shock protein (Hsp) 10 fused at its 3' end to HPV16 E7 protein. The fusion protein is used in the method of the invention. The

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ADT7511
ID ADT75
XX ADT71
XX FVe p
XW CYtos
XW Inman
XW Inman
XW Inman
XX ADT8
AN OCION
XX COION
XX COION
XX COION
XX Plamm
OS Flamm
OS Flamm
OS Flamm
OS Chime
XX COION
XX ADT8
AN WO200
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; respiratory-Gen; antiasthmatic; vaccine; immunomodulator; immune response; atopic disease; allergy; seasonal respiratory allergy; perennial respiratory allergy; allergy; rhinitis; hayfever; nonallergic rhinitis; vasomotor rhinitis; irritant rhinitis; grass pollen allergy; weed pollen; tree pollen; animal danders; allergic asthma; food allergy; house dust mite allergy; fungal spore; cancer; tumour progression; T cell lymphoma; melanoma; lung cancer;
                                                                                                                                                                     New Fve polypeptide that is a fragment, homologue, variant or derivative of Fve protein and that comprises a biological activity of native Fve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004092210-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fve polypeptide; antiallergic; antiinflammatory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Fve fusion protein mutant sequence #48.
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                              This invention relates to a novel Fve (Flammulina velutipes) polypeptide
                                                                                          Claim 6;
                                                                                                                                                                                                                                                                                                                                                   Chua KY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-2003; 2003GB-00008988
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                                                                                                                                                                                                                                                               2004-758336/74.
DB; ADT75832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; breast cancer; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                Seow SV,
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                                                                                    286pp;
                                                                                                                                                                                                                                                                                                                                                                                                          TECHNOLOGY & RES.
                                                                                                                                             preventing and treating
                                                                                                                                                                                                                                                                                                                                                   Kolatkar PR;
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                                                                                    English
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Pred. No. 5.3e-57;
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                                                                                                                                             allergy
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E6/E7 fusion protein from

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ID AXY25375
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KW immun
KW HPV a
XX Synth
OS Human
XX W0993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc prophylaxis of a disease, for the preparation of a pharmaceutical composition for the treatment of a disease, such as an acopic disease or cc composition for the treatment of a disease, such as an acopic disease or can allergy (for example seasonal respiratory allergy, perennial cc respiratory allergy, allergic rhinitis, hayfever, nonallergic rhinitis, respiratory allergy against grass pollen, conserved and the pollen or animal danders, an allergy against grass pollen, concercic astima, food allergy or an allergy to a house dust mite from cc allergic astima, food allergy or an allergy to a house dust mite from cc proglyphidae, preferably Blomia tropicalis or from Family concerns to preferably permatophagoides preferably permatophagoides for treating or preventing cancer or in suppressing tumour progression, where the cancer comprises a cc cancer or in suppressing tumour progression, where the cancer comprises a cc rell lymphoma, melanoma, lung cancer, colon cancer, breast cancer or prostate cancer. The present sequence is that of a gene which encodes a colon colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV fusion protein D1/3-E7-His(HPV16).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; prevention; treatment
                                                                                               1999-405485/34.
DB; AAX78791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   papillomavirus.
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usion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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96.9%;
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Pred. No. 5.8e-57;
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Best Local :
This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce a immune response in a patient to an HPV antigen. They can also be used preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                              Disclosure; Fig 1; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-190587/16.
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                                                                                                                                                                                                                                                                                                                                                                                   AAX29780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITHKLINE BEECHAM BIOLOGICALS
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein; protein D; vaccine; immunotherapy;
enign; malignant; virus; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delisse AEF,
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Pred. No. 6.1e-57;
0; Mismatches 3
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Matches

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RESULT 48
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Best Local
                                                       Query Match
                                                                                                                                                                                 The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 220 AA;
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                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AED52632.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrrell
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                              Local
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  95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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Score 512; DB y; Pred. No. 6.1e-57;
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Pred. No. 6.1e-57;
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                                                 Length 220;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAX75375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce arimmune response in a patient to an HPV antigen. They can also be used f preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response; HPV antigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising induce immune response
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N-PSDB; AAX78796.
17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1997;
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                                                 AAY02636;
                                                                                                  AAY02636 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                          1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 230
                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                         WHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein CLYTA-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-00027262.
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to HPV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 512; DB 2;
Pred. No. 6.8e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E7 or E6/E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239;
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                                                                                                                                                                                                  RESULT 51
                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLYTA-E7-His protein
                       Human papillomavirus Synthetic.
                                                                                                                                                    AED52644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX29785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1999
                                                                    Fusion protein; vaccine; papilloma;
virucide; uterine cervix tumor; E7;
                                                                                                      Fusion protein cLytA-E7-His/HPV16.
                                                                                                                             29-DEC-2005
                                                                                                                                                                            AED52644 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lombardo-Bencheikh
                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK)
                                                                                                                                                                                                                                                                                                                              Local Similarity
les 95; Conserv
                                                                                                                                                                                                                                     193
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                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          benign;
                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                               239 AA;
                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6; E7; fusion protein; CLYTA; vaccine; enign; malignant; virus; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                             (first entry)
                                               pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97GB-00017953
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                                                                                                                                                                                                                                                                                                                                         99.0%;
                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                                                                                                                                                                                                                                                                Score 512; DB 2; 1
Pred. No. 6.8e-57;
0; Mismatches 3;
                                                                                                                                                                            ₹
                                                                                 cytostatic; papillomavirus infection;
                                                                       LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerard CMG;
                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                      Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunotherapy;
                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                            Smith L,
                                                                                                                                                03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                        02-OCT-2003; 2003WO-US031726.
                                                                                                                                                                                                                                                                       15-APR-2004.
                                                                                                                                                                                                                                                                                                                            WO2004030636-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of an E7E6 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO44066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO44066 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 11; Fig 12; 96pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
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                                                                                       (AMHP ) WYETH HOLDINGS CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                               Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive system cancer; penile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97EP-00179535
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Pred. No. 6.8e-57;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lower gastrointestinal tract cancer; penile cancer; vulvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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RESULT 53
AAY43480
THE FIRST SOLUTION AND AND SOLUTION AND SOLU
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Best Local :
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27-AUG-2003
26-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTLA4; E7; fusion protein; B7 receptor positive B cell; CTLA4 receptor positive T cell interaction; immune syst autoimmune disease; lupus erythematosus; host-graft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY43480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system, including penile and vulvar cancer.
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                                                                                                                 US5968510-A
                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplant rejection; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a CTLA4-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY43480 standard; protein; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 72-73; 101pp; English.
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                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents an E7E6 fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                          /note= "leader sequence"
27. .155
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%;
                                                                                                                                                                           "E7 sequence"
                                                                                                                                                                                                                              "CTLA4 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۰;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 512; DB 8; 1
Pred. No. 7.1e-57;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interaction; immune system; nematosus; host-graft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E7 polypeptides, (HPV) -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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19-OCT-1999

04-OCT-1996;

96US-00725776

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AAYOLT 54
AAYOLT 52
ID AAYOL
XX AAYOL
AC AAYOL
XX 26-MA
DT 26-MA
XX CTLA4
XW CTLA4
XW SOLUM
XX SOLUM
XW SOLUM
XX SOLUM
X
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1991;
22-JAN-1993;
15-APR-1994;
18-JAN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a soluble CTLA4 fusion protein, for use in the method of the invention. The specification describes a method for regulating CTLA4 receptor positive T cell interactions with B7 receptor positive B cells. The method comprises contacting the CTLA4-positive T cells with monoclonal antibody fragments reactive with CTLA4. This inhibits (and therefore regulates) interactions between CTLA4 positive T cells and B7 positive B cells. The method may be used for regulating CTLA4 receptor positive T cell interactions with B7 receptor positive B cells. In this way the immune system of an individual can be manipulated (especially suppressed) for the treatment of autoimmune diseases (especially lupus erythematosus) and to prevent host-graft and transplant rejection. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-
                                                                                                                                                                                                                                                                        immune system disease; graft versus host disease; psoriasis; graft transplant rejection; T cell lymphoma; benign lymphocytic angiltis; autoimmune disease; lupus erythematosus; Grave's disease; Addison's disease; Crohn's disease; multiple sclerosis; ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease; viral proliferation; T cell activation; AIDS; HTLV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen; soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253
   08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino terminal CTLA4-carboxy terminal E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY01502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01502 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 37; 75pp; English.
                                                            23-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTLA4 positive T cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00723617.
93US-00008898.
94US-00228208.
95US-00375390.
95US-00465078.
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   97US-00889666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 512; DB 2;
Pred. No. 7.3e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kiener PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linsley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
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RESULT 55
AAW97612
ID AAW97612
AC AAW97
XX AM97
XX 26-M9
DT 26-M9
XX CTLA4
XW CTLA4
KW SOlub

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC protein which is reactive with the B7 antigen. DNA encoding the CTLA4 CC protein can be used in a vector in a host vector system for producing soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell cinteractions with B7 positive cells. The CTLA4Ig fusion protein can be used for treating immune system diseases mediated by T cell interactions with B7 positive cells. The immune system diseases include graft versus constitute cells. The immune system diseases include graft versus that disease, psoriasis, immune discrets associated with graft cransplant rejection, T cell lymphoma, benign lymphocytic angilits, and autoimmune disease such as lupus erythematosus, Grave's disease, Caddison's disease, Crohn's disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome, and mixed connective tissue disease. The Cusion protein may also be used to block the proliferation of viruses tission of relativation, such as the virus that causes AIDS, Chilvi. The present sequence was created in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1991;
22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen; soluble CTLA4; T cell interaction; B7 positive cell; immune disorder; immune system disease; graft versus host disease; psoriasis; graft transplant rejection; T cell lymphoma; benign lymphocytic angiit autoimmune disease; lupus erythematosus; Grave's disease; Addison's disease; Crohn's disease; multiple sclerosis; ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease; viral proliferation; T cell activation; AIDS; HTLV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-228484/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino terminal CTLA4-carboxy terminal E7 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW97612 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kiener PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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93US-00008898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 2; 1
Pred. No. 7.3e-57;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linsley
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the CTLA4
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23-MAR-1999 US5885796-A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion components of the protein which is reactive with the B7 antigen. DNA encoding the CTLA4 protein can be used in a vector in a host vector system for producing soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell interactions with B7 positive cells. The CTLA4Ig fusion protein protein can be used for treating immune system diseases mediated by T cell interactions with B7 positive cells. The immune system diseases include graft versus host disease, psoriasis, immune disorders associated with graft transplant rejection, T cell lymphoma, benign lymphocytic anglitis, and autoimmune diseases such as lupus erythematosus, Grave's disease, Cohn's disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome, and mixed connective tissue disease. The fusion protein may also be used to block the proliferation of viruses dependent on T cell activation, such as the virus that causes AIDS, THIVI. The present sequence was created in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
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15-APR-1994;
18-JAN-1995;
                                                                                                                                                        Monoclonal antibody; MAb; extracellular domain; CTLA4; B7 antigen; T cell interaction; inflammation; autoimmunity; transplantation; GCH neoplasia; infectious disease; graft versus host disease; psoriasis; immune disorder; lymphoma; leukemia; autoimmune disease; arthritis;
   07-JUN-1995;
                                                                                                                                            diabetes mellitis;
                                                                                                                                                                                                                                        CTLA4/E7 fusion protein.
                                                                                                                                                                                                                                                                       24-JAN-2000
                                                                                                                                                                                                                                                                                                                                   AAY41132 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 253
                                 02-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTLA4 receptor protein for use in treatment of immune system diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-228535/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1995;
                                                               US5977318-A
                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brady W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       (first entry)
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93US-00008898.
94US-00228208.
95US-00375390.
   95US-00488062
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                                                                                                                                            oncostatin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ledbetter JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 2; L
Pred. No. 7.3e-57;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                          CTLA4 receptor; CTLA4-Ig; fusion protein; B7 extracellular domain; human; immunoglobulin; autoimmune disease; cancer; viral infection;
                                                                                                                                                             05-FEB-1999
                                                                                                                                                                                                                             AAW81586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                         CTLA4/E7 fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 37; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New anti-CTLA4 monoclonal antibodies, used for treating e.g. inflammation, autoimmunity, transplant rejection, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
95; Conserv
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                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00723617.
93US-00008898.
94US-00228208.
95US-00375390.
                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Damle NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 512; DB 2; 1 Pred. No. 7.3e-57; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linsley PS,
                                                            antigen; hinge; CH2; CH3;
T cell; immune system;
E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ledbetter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 253;
                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Human papillomavirus

Homo sapiens

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RESULT 58
AAW87562
ID AAW87
XX AAW87
AC AAW87
XX O1-MP
CT O1-MP
CTLA4
XX CD28;
KW CD28;
KW CTLA4
XX CTLA4
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Best Local S
Matches 95
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22-JAN-1993;
28-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                            This represents a CTLA4/E7 fusion protein. The invention provides a CTLA4-II fusion protein that binds the B7 antigen and has a first amino acid sequence consisting of the extracellular domain of CTLA4 and a second amino acid sequence consisting of the hinge, CH2 and CH3 regions of a human immunoglobulin molecule. The fusion protein inhibits interaction of T cells with B7-positive cells and may be useful for treating immune system diseases, e.g. autoimmune diseases, cancer or viral infections. The present sequence is an example of such a fusion protein and contains an amino-terminal CTLA4 domain and aN E7 carboxy- terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion
system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Peptide
                     CD28; B7; fusion protein; hinge CH2; CH3; human IgC-gamma1; CTLA4; CTLA4 receptor; ligand; regulation; T-cell interaction; B7-positive cell;
                                                                                          01-MAR-1999
                                                                                                                   AAW87562;
                                                                                                                                         AAW87562 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 37; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-044666/04.
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            immune
                                                                CTLA4-E7
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                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                      61
             system disease.
                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of CTLA4 and immunoglobulin fragment - disorders.
                                                                                                                                                                                                                                                                                                                                                                       253
                                                                fusion protein.
                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                  MHGDTFTLHEYMLDLQPETTDLYXXXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linsley PS,
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                      Ŗ,
                                                                                         (first
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93US-00008898.
93US-00069693.
94US-00228208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CTLA4 partial sequence"
27. .154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .26
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/note= "E7 partial sequence"
155. .253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "E7 carboxy terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                         entry)
                                                                                                                                                                                                                                                                                                                             99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CTLA4 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                            253
                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                Score 512; DB 2; Pred. No. 7.3e-57; 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ledbetter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terminal domain"
                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating
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Matches
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Best Local Similarity
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22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a CTLA4-E7 fusion protein. CTLA4 is a receptor protein having a high degree of homology with CD28. The CTLA4 receptor is identified as a ligand for the B7 antigen. The CTLA4 protein can also be used to construct a fusion protein of CTLA4 and human can also be used to passed. The CTLA4 protein was fused to the hinge CH2 immunoglobulin (IG)-gammal. The CTLA4 protein was fused to the hinge CH2 and CH3 regions of human IgC-gammal. Soluble CTLA4-Ig fusion proteins can be used to regulate T-cell interactions with B7-positive cells and to
                                     preM protein; C protein; NS1 protein signal; vaccine;
viral disease; antigen; dendritic cell; immune respon
                                                cytostatic; virucide; dengue virus; recombinant replicon; preM protein; C protein; NS1 protein signal; vaccine; cerv
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             treat immune system diseases mediated by such interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble CTLA4 protein that binds B7 antigen of activated B cells fusion proteins useful for regulating T-cell interactions with B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                     Human papillomavirus type 16
                                                                                                                18-NOV-2004
                                                                                                                                        ADR47005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Fig 37; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1995;
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                                                                                                                                                                                                                                                                                   156
                        papillomavirus
                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQABPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                  standard;
                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDELDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                               (first entry)
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93US-00008898.
94US-00228208.
95US-00375390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brady W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00459818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. .155
                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "E7 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Damle NK,
                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                  256
                                                                                        E7
                                                                                                                                                                                                                                                                                                                                    Score 512; DB 2;
Pred. No. 7.3e-57;
0; Mismatches 3
                                                                                     protein for Dengue virus vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kiener PA,
                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                 253
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                                                   cervical
                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells.
                                                                                                                                                                                                                                                                                     215
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Human

papillomavirus type

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AEF40157
ID AEF4
XX
AC AEF4
AC AEF4
AC AEF4
XX
DT 23-M
XX
VACC
XW
VACC
XW
VACC
XW
Neop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC A dengue virus recombinant replicon has a deletion of the complete coding CC sequence for preM protein of dengue virus and also includes elements of CC e.g. the non-coding region in the whole of the 5'-end, the coding region of the front 20 amino acids in the C protein, and the coding region of CC NS1 protein signal; coding regions of all non-structural proteins. The C obtained vaccines are useful in producing preventives or/and remedies for CC cancer like cervical cancer and viral diseases. Such vaccines can CC virus can infect dendritic cells, and can effectively present antigen to CC repeatedly produce efficient timmune response thereby strengthening the CC repeatedly produce efficient immune response thereby strengthening the CC provide immunity effect. Different types of dengue virus can be used to CC repeatedly produce efficient immune response thereby strengthening the CC control of the companies were prepared by using a gene-CC expressing system using of the full-length dengue virus cDNA clone (CRS/FLD2). The recombinant virus vectors were transfected into baby conclusing sequence corresponds to the HPV type 16 E7 protein whose CC encoding gene is used as the gene of interest in the recombinant replicon
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding gene is of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus-like particle vaccines containing dengue virus recombinant replicon as core for carrier, applicable in preventives or/and remedies for tumors like cervical cancer and viral diseases.
                Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic; neoplasm; viral infection; virucide; infection; oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003; 2003CN-00115272.
30-JAN-2003; 2003CN-00115273.
                                                                     Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
                                                                                                          23-MAR-2006
                                                                                                                                           AEF40157
                                                                                                                                                                             AEF40157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 2; 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SHAN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2004; 2004WO-CN000088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004072274-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BEIJ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2004-625870/60.
DB; ADR47004.
                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                        (first entry)
                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 512; DB 8; Length 256; Pred. No. 7.4e-57; O; Mismatches 3; Indels
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RESULT 61
AAR97561
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a virus-like particle (VLP) vaccine which contains dengue virus (DEN) recombinant replicon as its core. The DEN replicon contains exogenous nucleotide sequences such as human papillomavirus (HPV) antigen proteins, immune regulators or combination of HPV antigen and immune regulators. The invention is useful for producing a drug for the prophylaxis and treatment of cancer or viral infection. The present sequence is a human papillomavirus oncoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003; 2003CN-00115272
30-JAN-2003; 2003CN-00115273
30-JAN-2004; 2004WO-00072274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 256 AA;
                     20-DEC-1994;
                                                                                                                                                                                                    27-AUG-2003
11-JAN-1997
                                                                                                                                                                                                                                       AAR97561;
                                                                                                                                                                                                                                                              AAR97561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2006-109169/11.
N-PSDB; AEF40156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
                                                                     27-JUN-1996.
                                                                                                                  Human papillomavirus
                                                                                                                                           humoral
                                                                                                                                                    Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
                                                                                                                                                                             Human papilloma virus E6/E7 protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing a drug for the prophylaxis and treatment of cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-2005; 2005US-00192923
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                                            20-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                       1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                      95;
 CSL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                          immune response; cellular
                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                                   (revised)
(first entry)
                       94AU-00000157
                                              95WO-AU000868
                                                                                                                                                                                                                                                              protein; 266
                                                                                                                                                                                                                                                                                                                                                                                                                                96.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 512; DB 10;
Pred. No. 7.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                          ımmune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 256;
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ARESULT 62
AAU02129
ID AAU02229
AC AAU02
AC AAU0
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C- terminal, or is a full length E6 molety fused to a full length E7 molety. The variant optionally has a linkage molety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF; chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ET antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;
New chimeric polypeptide, useful as anti-tumor vaccines, comprises carboxy terminal fragment of heat shock protein, Flt-3 ligand or
                                                                                                                                                                                                                                                                20-OCT-1999; 99US-00421608.
09-FEB-2000; 2000US-00501097.
                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200129233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flt-3 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 266 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwards SJ,
                                                                                          WPI; 2001-290921/30
                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000; 2000WO-US041422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunotherapy.
                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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DB; AAT31833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, pref. infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cox J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FL) used to make chimeric immunogenic polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 512; DB 2;
Pred. No. 7.8e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to treat
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ARBSULT 63
AAB31615
ID AAB31
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DT 30-AE
XX Heat
XX E7 mp)
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 19; 110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of Hsp65-E7 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB31615 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
                                                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                 10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               well as humans, and have low immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and useful for administration to domesticated or agricultural animals,
                                                                                                              (STRE-) STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents the amino acid sequence of Flt-3 ligand (FL) used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                          99US-0143757P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 4;
Pred. No. 8.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                  CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Siegel M,

Chu NR,

Mizzen LA

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RESULT 64
AAB31613
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a fusion protein comprising Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The station describes a method of determining whether a compound stimulates a Th1-like response. Th1 calls are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; glutathion-S-transferase; GST; E7 protein.
                                                                                                     Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
 Example 10;
                                    Screening
                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB31613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB31613 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening
                        lymphocyte
                                                                                                                                                                                   10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                             18-JAN-2001.
                                                                                                                                                                                                                                       WO200104344-A2
                                                                                                                                                                                                                                                                Human papillomavirus.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 12; Fig 11; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for compounds that stimulate Th1-like responses in CD4+ {	t T}
                                                                                                                                  (STRE-)
                                                                 2001-138361/14.
DB; AAF25016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-138361/14.
DB; AAF25022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                  STRESSGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                          for compounds that stimulate Th1-like cells.
                                                                                                      Chu NR,
Fig 9; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA,
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                          99US-0143757P
                                                                                                                                  BIOTECHNOLOGIES
                                                                                                      Mizzen LA
                                                                                                                                                                                                                                                                                                                                                                     of glutathion-S-transferase
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 English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 512; DB 4;
Pred. No. 8.9e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                      responses
                                                                                                                                                                                                                                                                                                                                                                      (GST) -E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                            cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257
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ARDSULT 65
ARD22926
ID ARD22
XX ARD22
XX ARD22
XX Unide
XW fusic
XW fusic
XW Chime
XX Chime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a glutathion-S-transferase (GST) linked to HBV16 E7 protein, for purification purposes. The E7 protein was used to construct a fusion protein with Mycobacterium bovis heat shock proteins (Hsp). The fusion proteins are used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprises contacting naive lymphocytes in the detecting the TH1-like response exhibited by the cell sample. The protein detecting the TH2-like response exhibited by the cell sample. The protein which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion partner; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 324 AA;
                                                                                                                                          Disclosure;
                                                                                                                                                                                                                    A new DNA sequence encoding a fusion protein comprising a mutagenized H (human papillomavirus) E6 or E7 coding sequence and a sequence encoding highly immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virucide; cytostatic; E6; E7 fusion fusion partner; immunogenicity; HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HbsAg-EE7T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                            Cid-Arregui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001EP-00107271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001EP-00107271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1243655-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogens
                                                                                                                                                                                                  infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                          2002-724952/79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                               AAL53424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein
                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Zur Hausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity;
                                                                                                                                       34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
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Pred. No. le-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; HPV; immunogenic; vaccine;
infection; neoplasm; HbsAg-EE7T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                       VAH
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The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced codons which lead to enhanced translation in a mammalian cell, containi a mutation which results in production of a truncated non-functional

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Matches
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                                                                                                                                                                                                                                       encoding
encoding
The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic acid vector comprising a first sequence encoding an antigenic polypeptid or peptide, and optionally, a second sequence linked to the first sequence and encoding an immunogenicity-potentiating polypeptide (IPP); and a second nucleic acid vector encoding an anti-apoptotic polypeptide. When the second vector is administered with the first vector to a subject, a T cell mediated immune response to the antigenic polypeptide or peptide is induced that is greater in magnitude and/or duration than an immune response induced by administration of the first vector alone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammallan host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the HbsAg-BE7T fusion protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2003; 2003US-0449429P.
18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus Synthetic.
                                                                                                                                                                                      Disclosure; SEQ ID NO 18; 158pp; English
                                                                                                                                                                                                                                                                          New nucleic
                                                                                                                                                                                                                                                                                                        N-PSDB; AEA40827
                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2005.
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                                                                                                                                                                                                                        inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2004; 2004WO-US005292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2005047501-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-apoptotic vector E7-BCL-xL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEA40828 standard;
                                                                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                          2005-367009/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                    eic acid composition comprising a first nucleic acid vector
an antigenic polypeptide and a second nucleic acid vector
an anti-apoptotic polypeptide, useful as an immunogen for
ng the growth of a tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nicity; immunogenicity-potentiating polypeptide; IPP; T-cell;
immune stimulation; tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                           Kia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 5
Pred. No. 1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention further includes: a particle comprising a material that is suitable for introduction into a cell or an animal by particle bombardment, bound to which is the first and second vectors or composition; a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response, comprising the particle and a carrier or an excipient; inducing or enhancing an antigen specific immune response in a subject; increasing the numbers of CDB+ CTLs specific for a selected desired antigen in a subject; and inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as an immunogen for inhibiting the growth of a tumor, hence it has cytostatic activity. This sequence represents ananti-apoptotic vector E7-
                                                                                                                                                                                                                                                       24-FEB-2003;
18-JUL-2003;
31-DEC-2003;
                                                                                                    New nucleic acid composition comprising a first nucleic acid vector encoding an antigenic polypeptide and a second nucleic acid vector encoding an anti-apoptotic polypeptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                                  Wu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 349 AA;
                                                                                                                                                                                                                                                                                                           24-FEB-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEA40831
                                                                                                                                                                         WPI; 2005-367009/37.
                                                                                                                                                                                                                                                                                                                                       26-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                  WO2005047501-A1
                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-apoptotic vector E7-mtBCL-xL
                                                                                                                                                                                                                             (UYJO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein of the invention.
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                                                                                                                                                                                                                            VIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                    CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                       2003US-0449429P.
2003US-0488527P.
2003US-0533792P.
                                                                                                                                                                                                                             JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                              2004WO-US005292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity-potentiating polypeptide; IPP; T-cell;
stimulation; tumor; cytostatic.
                                                                                                                                                                                                    Ki m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512; DB 9;
Pred. No. 1.1e-56;
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The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic acid vector comprising a first sequence encoding an antigenic polypeptide or peptide, and optionally, a second sequence linked to the first sequence and encoding an immunogenicity-potentiating polypeptide (IPP);

Disclosure;

SEQ ID NO

21; 158pp; English.

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RESULT 68
AX25377
ID AAY25
XX AAY25
XX AAY25
XX Pusio
KW Fusio
KW immun
KW HPV a
XX IMMAN
XX IMMAN
XX IMMAN
XX IMMAN
PD 08-JU
XX 18-DE
XX 24-DE
XX X IMI
PR 24-DE
XX X IMI
PR 18-DE
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PR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally
                                                                                                                                                                                                           Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                               WPI; 1999-405485/34.
N-PSDB; AAX78793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response; HPV antigen; prevention; treatment.
                                                                                                                                       Example III; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV fusion protein D1/3-E6E7-His/HPV16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                                                                                                                                       , PIW
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                                                                                                                                       50; 62pp; English
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                                                                                                                                                                                                           an E6, E7 or E6/E7 to HPV.
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Pred. No. 1.1e-56;
0; Mismatches 3
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                                                                                                                                                                                                                                           fusion protein from HPV
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RESULT 69
AAY02633
ID AAY02
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Best Local S
Matches 95
                    This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce simmune response in a patient to an HPV antigen. They can also be used preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                    Bruck C, Cabezon S
Lombardo-Bencheikh
Sequence 371 AA;
                                                                                                                                            Disclosure; Fig 6; 95pp; English.
                                                                                                                                                                     treatment or prophylaxis
                                                                                                                                                                                      Human Papilloma Virus (HPV)
                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric; E6; E7
tumour; lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prot.D1/3-E6-E7-His/HPV16 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003
22-JUN-1999
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                                                                                                                                                                                                                                                                                                                       22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   WO9910375-A2
                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                           1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                  Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E7; fusion protein; protein n; benign; malignant; virus;
                                                                                                                                                                                                                                                                                                                       97GB-00017953
                                                                                                                                                                                                                                                                                                                                                98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                benign;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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                                                                                                                                                                                                                                                                   Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371
                                                                                                                                                                      fusion proteins - useful in vaccines HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 512; DB 2;
Pred. No. 1.2e-56;
0; Mismatches 3
                                                                                                                                                                                                                                                                  Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D; vaccine;
infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy;
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Query Match Best Local Matches

95;

Similarity

99.0%; milarity 96.9%; Conservative

0

Score 512; DB 2; 1 Pred. No. 1.2e-56; 0; Mismatches 3;

Length 371;

Indels

<u>,</u>

Gaps

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RESULT 70
AED52638
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                                                                                                   Best Loc
Matches
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                                                                                                                                                                                           The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AED52638 standard; protein; 371
                                                                                                                                                        Sequence 371
                                                                                                                                                                                                                                                                                                                                Example 6; Fig 6; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                            Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fugion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein D1/3-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AED52638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae; strain 772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide; uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                      2005-557648/57.
DB; AED52637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 362
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325
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                                                                                                      95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                   Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 362
             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                   MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 16.
                                                                                                                 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     papilloma; cytostatic; papillomavirus infection;
tumor; E7; D protein.
                                                                                                   Score 512; DB 9;
Pred. No. 1.2e-56;
0; Mismatches 3
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                                                                                                                              Length 371;
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                        98
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RESULT 72
AAY02637
ID AAY02
XX AA02
XX 17-OC
DT 17-OC
DT 22-JU
XX
DE CLYTA
XX
KW Chime
KW 1esio
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                         AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an 86 or 87 protein or 86/87 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein; E6 protein; E7 protein; E6/E7; immu immunological fusion partner; CpG oligonucleotide; HPV antigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY25381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY25381 standard; protein; 390 AA
                                                               17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                  Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-405485/34.
N-PSDB; AAX78797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPV fusion protein CLYTA-E6E7-His/HPV16
Chimeric; E6; E7; fusion protein; CLYTA; vaccine; lesion; benign; malignant; virus; infection.
                                      CLYTA-E6E7-His protein.
                                                                                                       AAY02637;
                                                                                                                               AAY02637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example VIII; Page 55-56; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dalemans
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                                                                                                                                                                                                                                                                                                Local Similarity
es 95; Conserv
                                                                                                                                                                                            344
                                                                                                                                                                                                             61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLJ,
                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 381
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; E6 protein; E7 fusion partner; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-00027262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-EP008563
                                                                                                                            protein; 390
                                                                                                                                                                                                                                                                                                           99.0%;
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                                                                                                                                                                                                                                                                                                              Score 512; DB 2; Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E7 or E6/E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; E6/E7;
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator; tumour;
                                                                                                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                   Indels
              immunotherapy; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from HPV
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                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 73
ARD52646
ID ARD52
XX ARD52
XX Pusio
XX Fusio
XX Fusio
XX Fusio
XX Fusio
XX Ingal
Control
XX Strep
OS Strep
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Best Local (
                                                                                                     Streptococcus pneumoniae. Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                   rusion protein;
virucide; uterir
                                       04-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus.
Streptococcus pneumoniae.
Chimeric.
              24-AUG-1998;
                                                              IN9801903-I4
                                                                                                                                                                                           Fusion protein cLytA-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 390
                                                                                                                                                                                                                    29-DEC-2005
                                                                                                                                                                                                                                            AED52646;
                                                                                                                                                                                                                                                                      AED52646 standard; protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 14; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Papilloma Virus (HPV) fusion proteins - useful in vaccines treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruck C, Cabezon Silva Lombardo-Bencheikh A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                      uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,
                                                                                                                                                                                                                   (first entry)
               98IN-CH001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-00017953.
                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-EP005285
                                                                                                                                                      accine; papilloma; cytostatic;
cervix tumor; E7; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512; DB 2;
Pred. No. 1.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 390;
                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                 papillomavirus infection;
                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 74
AAM50663
ID AAM50
XX AAM50
XX 29-AU
DT 29-AU
DT 08-AP
XX Thior
XX Thior
XX Thior
XX Chime
XX Chime
XX Chime
YT Prote
FT Prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (cLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM50663 standard; protein; 421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                  WO200200892-A1
                                                                                                               Protein
                                                                                                                                             Cleavage-site
                                                                                                                                                                          Protein
                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                       Chimeric.
                                                                                                                                                                                                                                                                                                  Homo sapiens
Escherichia
                                                                                                                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                   Thioredoxin; ubiquitin;
                                                                                                                                                                                                                                                                                                                                                                                                Thioredoxin-ubiquitin-ProteinD1/3 E7-His triple fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2003
08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM50663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12;
                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2005-557648/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSBEBEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 14; 96pp;
                                                                                                                                                                                                                                                                                                      coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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                                                                                                                                                                                                                        /label= Thioredoxin
                                                              'label= Histidine_tail
                                                                                               /label= ProteinD1/3-E7
                                                                                                                              label=
                                                                                                                                                             /label=
                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                        ocation/Qualifiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%;
                                                                                                               .412
                                                                                                                                                                            .199
                                                                                                                                                                                                           . 125
                                                                                                                                               . 202
                                                                                                                           UBP1_cleavage_site
                                                                                                                                                          Ubiquitin
                                                                                                                                                                                                                                                                                                                                                                 proteinD1/3 E7; tumour; antigen; cancer; vaccine;
                                                                                                                                                                                         Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 512; DB 9;
Pred. No. 1.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 390;
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RESULT 75
AAB31610
ID AAB31
XX AAB31
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The present sequence is that of a triple fusion protein comprising, from CC the N-terminal end, Escharichia coli thioredoxin, human ubiquitin and CC than papillomavirus proteinni/3 E7, followed by a histidine affinity CC tail. The triple fusion protein was produced in E. coli GI724 host cells CC transformed by an expression vector comprising DNA (see ABA9128) CC encoding the fusion. This is an example of the production of triple CC fusion proteins of the invention that comprise ubiquitin fused between CC thioredoxin and a protein of interest, in this case ProteinDi/3 E7. A CC claimed method of producing a recombinant protein of interest involves: CC column and a host cell (preferably E. coli) under conditions which allow CC co-expression of the triple fusion and a ubiquitin-specific endoprotease CC (especially uBpl from Saccharomyces cerevisiae); and recovering the CC recombinant protein directly from the bacterial cells after it has been CC subjected to the action of the ubiquitin-specific endoprotease in vivo. CI In the present case, expression is controlled by the addition of tryptophan. The recombinant protein can used as a vaccine for cancer CC therapy. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-147888/19.
N-PSDB; ABA91285.
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30-OCT-2000; 2000GB-00026484.
   18-JAN-2001
                                                                                                                          Mycobacterium tuberculosis.
Human papillomavirus.
                                                                                                                                                                                                                                                                                      Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of Hsp40-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB31610 standard; protein; 493
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                                                                WO200104344-A2
                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
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ΑΑ;
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Pred. No. 1.4e-56;
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RESULT 76
AAB03790
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Best Local
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06-AUG-2003
13-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a fusion protein comprising a Mycobacterium tuberculosis heat shock protein (Hsp) 40 fused at its 3' end to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Thi cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock protein; tumour specific antigen; colibacillus; microzyme; plant; immune response; tumour; cancer; human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB03790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB03790 standard; protein; 638
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                           24-SEP-1998;
                                                                              24-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogens
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                                                                                                                                                                                                CN1248631-A
                                                                                                                                                                                                                                                          Chimeric.
                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                      pointed condyloma.
                                                                                                                                       29-MAR-2000
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                                                                                                                                                                                                                                                                               papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein and tumour specific antigen fusion protein sequence
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(revised)
(first entry)
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                           98CN-00112264
                                                                                 98CN-00112264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 512; DB 4;
Pred. No. 1.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 493;
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RESULT 77
AAB31609
ID AAB31
XX AAB31
XX AAB31
XX AAB31
XX Heat
XX Heat
KW Llymph
KW E7 px
XX Synt!
OS Mycob!
OS Humar
XX Hoge
OS Humar
XX Hoge
OS Humar
XX IS-JE
PF 10-JI
XX OB-JI
XX OB-JI
XX Siege
PF Siege
XX WPI;
DR WPI;
DR WPI;
XX Scree
PF 19mpi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific antigen of human papillomavirus (HPV). The fusion protein can be expressed in collbacillus, microzymes and plants. The fusion protein is used to make immunostimulant injections, as it can produce specific cell immune and humoral immune responses. It possesses prophylaxis and therapeutic capacity for preventing human papillomavirus (HPV) infection, but also can be used for immunotherapy of pointed condyloma, tumours and cancer caused by HPV. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 12-SEP-2003 to standardise OS field)
                                                         WPI; 2001-138361/14
N-PSDB; AAF25012.
                            Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                                                                                      10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                            Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a fusion protein, consisting of a heat shock protein of mycobacterium bovis (var. BCG) fused to a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Fig 1; 5pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion protein for immunotherapy of venereal disease a heat shock protein of Mycobacterium bovis.
                                                                                                                                                         08-JUL-1999;
                                                                                                                                                                                                                   18-JAN-2001.
                                                                                                                                                                                                                                               WO200104344-A2
                                                                                                                                                                                                                                                                         Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB31609 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-431995/38
             lymphocyte cells
                                                                                                                                (STRE-)
                                                                                                                                                                                                                                                                                        Mycobacterium bovis.
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                                                                                                                                STRESSGEN BIOTECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                  NR,
                                                                                                                                                           99US-0143757P
                                                                                                                                                                                                                                                                                                                                                                                          of Hsp65-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 3; L
Pred. No. 2.4e-56;
0; Mismatches 3;
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                                                                                                                                 CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fused to a tumour The fusion protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT 78
AAB31619
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein compriseing at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
The present sequence represents a fusion protein comprising a Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB31619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31619 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 639 AA;
                                                                                                                                   Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                                                                 N-PSDB; AAF25036.
                                                                                                                                                                                 WPI; 2001-138361/14.
                                                                                                                                                                                                                                                                       08-JUL-1999;
                                                                                                                                                                                                                                                                                                     10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogens
                                                                                         Example 15;
                                                                                                                                                                                                                                                                                                                                    18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
                                                                                                                     lymphocyte cells.
                                                                                                                                                                                                                                           (STRE-) STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                                                                                                                                                                                                                                                                           papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Fig 4A-B; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of Hsp65-E7 fusion protein.
                                                                                                                                                                                                           Chu NR,
                                                                                       Fig 15A-B; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
                                                                                                                                                                                                               Mizzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 512; DB 4; L
Pred. No. 2.4e-56;
Niematches 3;
                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 639;
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Best Local (
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                            The present sequence represents a fusion protein comprising a Aspergillus fundigatus heat shock protein (Hsp) 60 fused to a HPV16 E7 protein. The fusion protein is used in the method of fused in the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response whibited by the cell sample. The proteins which may be used in the method of the invention are Hsp55, Hsp40, Hsp50, and Hsp71. The method may be used to identify compounds that stimulate Th1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                       Example 16; Fig 16A-B; 88pp; English.
                                                                                                                                                                                                                                                     Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                                                                                                                                                                                                                                  Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus.
Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heat shock |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of Hsp60-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001.
                                                                                                                                                                                                                                      lymphocyte
                                                                                                                                                                                                                                                                                                                                                                  (STRE-) STRESSGEN BIOTECHNOLOGIES CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                   2001-138361/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                        cells
                                                                                                                                                                                                                                                                                                                                  Chu NR,
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                response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 512; DB 4;
Pred. No. 2.4e-56;
                  microbial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                pathogens
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ADP18635
ID ADP18
XX ADP18
XX ADP18
XX ADP18
XX HUMAN
XX HPV;
XX HUMAN
XX HO200
XX YOU
PD 30-OC
XX I YAR
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                                                                              The present sequence is the protein sequence of human papillomavirus E7 comcoprotein. E7 promotes oncogenesis through an inhibition of p21Cip21 cc transport into the nucleus. E7 abrogates Raf-associated arrest and CC prevents inhibition of cyclin E-CDK2 activity without disrupting Raf cc induction of p21Cip21. E7 neither interacts with p21Cip1 nor derepresses conduction of p21Cip21. E7 neither interacts with p21Cip1 nor derepresses conduction of p21Cip1 and cyclin E-CDK2 complexes. Raf down-regulates steady-cc state levels of Akt, a regulator of p21Cip1 localisation, leading to loss cof p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the cffects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. CC Maintenance of Akt activity is necessary and sufficient to bypass Raf carrest. The invention provides methods for identifying and using compounds capable of promoting the nuclear localization of p21Cip1. The methods can be used to inhibit aberrant cellular proliferation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV; oncoprotein E7;
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                                                                 treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2003; 2003WO-US012667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Westbrook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Query Match Best Local Similarity Matches 94; Conserv

Conservative

98.8%;

Score 511; DB 7; Pred. No. 2.9e-57; 1; Mismatches 3;

Length 98;

Indels

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Gaps

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98

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RESULT 81
ADO44064
                                                                                              CC The present sequence represents a fusion protein, comprising E6 and E7 CC polypeptides from human papillomavirus type 16 (HFP16). The fusion CC protein is designated E6E7PentM, and comprises an E6 amino terminus CC (where residues 63 and 106 have been replaced with glycine) and an E7 CC carboxy terminus (where residues 24, 26 and 91 have been replaced with CC glycine). E6E7PentM is representative of fusion proteins of the CC invention. The specification describes human papillomavirus E6 and E7 CC polypeptides, where the E7 polypeptide has mutations at any one or more CC of the amino acids corresponding to amino acids 24, 26 or 91 of the CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has CC mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of CC the invention are useful for treating or preventing human papillomavirus CC immune responses against HPV. They are also useful for treating lower content of the sequence of the securion for treating lower contents and they cancer of the sequence of the securion for treating lower contents and they cancer of the sequence of the securion proteins are useful for generating contents and they cancer of the sequence of the securion for treating lower contents and they cancer of the sequence of the sequence of the securior of the sequence of the se
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  Best Local Similarity Matches 94; Conserv
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                              Sequence 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 70-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2003; 2003WO-US031726.
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                                                                                                                                           reproductive
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    Conservative
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                                                                                                                                       tract cancers, e.g
system, including
                     98.8%;
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Score 511; DB 8;
Pred. No. 9.6e-57;
1; Mismatches 3
                                                                                                                                       , e.g. anal
ding penile
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                                                                                                                                       cancer, and other cancers of and vulvar cancer.
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                                             Length 248;
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MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

Matches

Conservative

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Score 510; DB 8; Pred. No. 1.3e-56; 1; Mismatches 3;

Length 248 Indels

0,

Gaps

0

Query Match Best Local Similarity

98.6%;

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RESULT 82
AD044062
ID AD044
AC AD046
AC AC AD046
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                                                          The present sequence represents a fusion protein, comprising E6 and E7 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E6E7TetM, and comprises an E6 amino terminus (where residues 63 and 106 have been replaced with glycine) and an E7 carboxy CC terminus (where residues 24 and 26 have been replaced with glycine). CC E6E7TetM is representative of fusion proteins of the invention. The CC specification describes human papillomavirus E6 and E7 polypeptides, CC where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers they they are also useful for treating lower gastrointestinal CC against they. They are also useful for treating lower gastrointestinal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
   Sequence 248 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 68-69; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004030636-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVGPICSQKP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHGDTPTLHEYMLDLQPETTDLYGYGQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of a fusion protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E7 polypeptides, (HPV) -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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                                                                                                                                                                                                                                                             The present sequence represents an B6E7 fusion protein, comprising wild crype B6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids 20, 26 or 91 of the sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                Matches
                                                                                                                                                                  Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer anal cancer; reproductive system cancer; penile cancer; vulvar cancer
                                                                                                                                                                                                                              Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO44060 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 67-68; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004030636-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of an E6E7 fusion protein
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DB; ADO44061.
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                       61
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                                                                                                                                            94;
                                                                                                                                                                    Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                    MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cassetti MC;
                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                             98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
                                                                                                                                            Score 509; DB 8;
Pred. No. 1.7e-56;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                       98
                                                                                                                                                                                     Length 248;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E7 polypeptides, (HPV) -associated
                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                              Gaps
                                                                210
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AAX50703
ID AAX50
ACC AAX50
AXX AAX50
AXX AAX50
AXX AAX50
AXX BT AAX50
AXX BT AAX50
AXX BT AAX50
AXX BT AAX50

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      SXEXEEXEX
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E7 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPV16 E7 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY50703
HPV 16E7
                                    06-AUG-2003
07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 25; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ24129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-023362/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus
                                                                                                  AAB49453;
                                                                                                                                        AAB49453 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic protein with altered biological function, useful for active immunization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 248
                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                           1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSBEBBBBBBBBAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٢
                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPRGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 98
                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenic; active
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jochmus
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                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 507; DB 3; Pred. No. 9.5e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Immune response; gene therapy; antigen presentation; vaccine; cancer;

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RESULT 86
AAO22639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The present invention relates to an expression vector comprising a CC promoter, signal sequences, an antigen, a cell-binding element, and a CC polyadenylation sequence. The expression vector can be used directly or CC after transduction of antigen-presenting cells, in vaccines for treatment CC and prevention of cancer, infections and autoimmune diseases. Vectors CC similar to the expression vector of the present invention, but expressing CC that contain MHC-II restricted epitopes for activation of CD4+ cells or CC elicitation of an immune response in vivo. The identified polypeptides CC (in APC) or vector containing DNA that expresses the polypeptides are Useful for treating the above conditions. The present sequence is HPV CC which hamper the secretion of the protein, which has a string of charged residues CC to result in the present protein, stablises the protein and facilitates CC secretion. The coding sequence for the present protein was used to CC construct the expression vector of the present invention. (Updated on 06-
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                           Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth; cancer; human papilloma virus; cervix; cell-mediated immune response;
                                                                                            HPV-16 protein
                                                                                                                         15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel vector expressing secreted antigen fused to cell binding element, useful in vaccines for treatment of e.g. cancer and infection, also
Human papilloma virus
                                                                                                                                                                                     AAO22639 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 17; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-007312/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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                                                                                                                                                                                                                                                                                                                                                                                         94;
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                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to correct
                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                         (first entry)
                                                                                         sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0132750P.
99US-0132752P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitopes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                      98.1%;
                                                                                          SEQ ID No
                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                       Score 507; DB 4; Length 98 Pred. No. 9.5e-57; 1; Mismatches 3; Indels
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                                                                                            26.
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 87
AAO22923
ID AAO22
XX AAO22
XX 12-DE
XX Virus
CKW Fusic
KW fusic
KW humar
XX humar
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XX 23-M2
PR 23-M2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for determining the possibility of recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV) or suspected of being infected with HPV, and has or had a (pre-)cancerous growth on or around the cervix. The novel method comprises incubating an E6 or E7 peptide of HPV with a sample from the patient, and assaying the sample for a cell-mediated immune response against the peptide. The method is useful for determining the possibility and preventing the recurrence of a (pre-)cancerous growth in a patient infected with HPV or suspected of being infected with HPV. The HPV E6 or E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence
                                                                                                                                                        Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine; fusion partner; immunogenicity; HPV infection; neoplasm; HPV16; human papillomavirus-16; EE7T-sequence.
                                                                                                                          Human papillomavirus.
                                                                                                                                                                                                                                                                                                                        AAO22923 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incubating the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2002; 2002WO-US023198
23-MAR-2001; 2001EP-00107271
                               23-MAR-2001; 2001EP-00107271.
                                                                                                                                                                                                                         Human papillomavirus-16 (HPV16)
                                                                                                                                                                                                                                                         12-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                          AA022923;
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                                                                25-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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Pred. No. 9.
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                                                                                                                                                                                                                       EE7T-protein sequence
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9.5e-57;
1es 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                     24-OCT-2003
25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing a mutation which results in production of a truncated non-functional protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the human papillomavirus-16 (HPV16) EB7T-protein sequence of the invention
                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a highly immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                             Human papillomavirus type 16.
                                                                                                                                                                                                                                                  Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 111 AA;
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 Boursnell MEG,
                                                   14-MAR-1991;
                                                                             10-MAR-1992;
                                                                                                       01-OCT-1992.
                                                                                                                                 WO9216636-A1
                                                                                                                                                                                                                                                                            HPV 16 E7 protein fragment.
                                                                                                                                                                                                                                                                                                                                                           AAR27724;
                                                                                                                                                                                                                                                                                                                                                                                    AAR27724 standard; protein;
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                          (IMMU ) IMMUNOLOGY LTD
                                                                                                                                                                                                                                       immunotherapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVIFCCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                    (revised)
(revised)
(first entry)
                                                   91GB-00005383
                                                                             92WO-GB000424
Inglis SC,
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                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%;
96.9%;
                                                                                                                                                         "start of HPV-16 E7 protein"
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                                                                                                                                                                                                                                                                                                                                                                                     262
 Munro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 507; DB 5;
Pred. No. 1.1e-56;
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RESULT 89
AAY08020
ID AAY08
XX AAY08
AC AAY08
AC
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using oligonucleotides SO5 and SO6. The prod. of the second reading frame is the HPV-16 E7 protein whereas the third reading frame encodes HPV-16 E6. The E6 and E7 ORPs are fused together to form a single continuous ORP via site directed mutagenesis and the immortilising potential of E7 is removed by altering two key codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites (pref. by inserting two sets of the DNA in opposite orientations to overcome the problem of intertypic recombination) to make a recombinant virus vector for use immunotherapeutically to activate cells of the immune system against HPV. See also AAR27723-43. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant virus vectors encoding human papillomavirus proteins - for treating and vaccinating against HPV infections and conditions caused them, such as cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L1 protein; capsomer; virus; vaccine; infection; treatment;
cervical carcinoma; fusion protein; anti-capsid; antibody; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2003
08-JUL-1999
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N-PSDB; AAQ29389.
                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus E7 protein.
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                                                                                                                                                                           Gissmann L,
                                                                                                                                                                                                                                                                                              06-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                      06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9918220-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                                   (LOYO ) UNIV LOYOLA CHICAGO
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                                                                                       1999-264026/22.
DB; AAX37567.
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                                                                                                                                                                           Mueller
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(first entry)
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Pred. No. 6.1e-56;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; prevention;
E7 protein;
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Human papilloma virus against HPV infection.

(HPV)

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fusion protein capsomers, used

in vaccines

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RESULT 90
ADJ32548
ID ADJ32
XX ADJ32
XX ADJ32
XX ADJ32
XX Integ
XX
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000;
24-OCT-2000;
12-OCT-2001;
15-MAR-2002;
                                                                                                             Reducing the proliferation of a cancer cell involves inhibiting ligand binding to an integrin receptor on the cancer cell, where the integrin
                                                                                                                                                                                                  WPI; 2004-154528/15.
N-PSDB; ADJ32547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003224993-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myeloma; carcinoma; glioma; plasmocytoma; sarcoma; thyoma; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin; cell proliferation; cancer; melanoma; adenoma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus (HPV) type 16 E7
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; 2000US-0242812P.
; 2001WO-US032127.
; 2002US-0365078P.
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Pred. No. 2.3e-56;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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Disclosure;

SEQ ID NO

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RESULT 91
AAB31607
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Best Local
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                      The present sequence represents the HPV16 E7 protein. HPV16 E7 was fused to a heat shock protein (Hsp), and used used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Thi cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprises contacting naive lymphocytes in the detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp40, Hsp40, and Hsp71. The method may be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                    Screening for compounds that stimulate lymphocyte cells.
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                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel M, Chu NR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of the HPV16 E7 protein
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DB; AAF25005.
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                                                                                                                                                                                                                                                                                                                                          3; Fig 2; 88pp; English.
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                          The invention relates to a novel composition comprising human papillomavirus (HPV) antigens or portions linked via hydrophobic bonds or mixed with very small size proteoliposomes (VSSP's). The invention further comprises a method for treating a tumor expressing an HPV antigen by administering an effective amount of this composition. The novel composition has cytostatic activity. The composition is useful for composition has cytostatic activity. The composition is useful for boosting the immune response against HPV antigens. The compositions are sultable for use in the pharmaceutical industry as vaccines in human therapeutics for cancer treatment. The cellular immune response against CHPV antigens is significantly boosted, especially with respect to cell cytotoxicity, ensuring that cells which exhibit the HPV antigen are CC destroyed more effectively. This sequence represents a Neisseria CC meningitidis Pl.7.16 delta 5 and HPV-16 E7 fusion protein, used in the CC expression of HPV antigens of the invention.
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Best Local :
                                                                                                                                                                                                                                                                                                   Vaccine composition for boosting cellular immune response against human papilloma virus (HPV) antigens, contains HPV antigens linked via hydrophobic bonds or mixed with very small size proteoliposomes (VSSP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2004; 2004WO-CU000010
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Torrens Madrazo IDC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
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                                                                                                                                                                                                                                                                         SEQ ID NO 7; 62pp; Spanish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
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Pred. No. 3.1e-56;
0; Mismatches 4
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Matches

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Best Local (
                                                                                The present sequence represents a fusion protein comprising Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                      Screening for compounds that stimulate Th1-like responses in CD4+lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-138361/14.
N-PSDB; AAF25019.
                                           Sequence 648
                                                                                                                                                                                                                                                                                                                                                                           Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp60; Hsp71; microbial pathogen;
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                                                                                                                                                                                                                                                           Example 11; Fig 10A-B; 88pp; English
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                           Chu NR,
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                                           AA,
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97.3%;
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Score 503; DB 4;
Pred. No. 3.5e-55;
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Pred. No. 2.5e-55;
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RESULT 95
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Mycobacterium tuberculosis.
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                                                                                                                                                                                                                             Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for compounds that stimulate Th1-like responses lymphocyte cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siegel M,
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                                                                                                                                                                                     Local
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                                                                                                                                                                       94;
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                                                        CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 98
                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                    Score 503; DB 4; Length 711; Pred. No. 4e-55; 0; Mismatches 4; Indels
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Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus.
Mycobacterium tuberculosis.
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                                                                               ABB81111 standard; protein; 99
                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for compounds that stimulate Th1-like responses in lymphocyte cells.
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DB; AAF25031.
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                                                                                                                                                                                                                                                                94;
                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                     724 AA;
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Pred. No. 4.1e-55;
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HPV E7 antigenic protein

05-NOV-2002

(first entry)

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ABB82376
ID ABB82376
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AC ABB82
XX AC ABB82
XX O8-J1
XX Immun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new nucleic acid molecule (I) encoding a first fusion polypeptide useful as a vaccine composition. (I) comprises a first nucleic acid sequence encoding a first polypeptide or peptide that promotes processing via the Major Histocompatibility Complex (MHC) class I pathway (MHC-I-PP) and/or promotes development or activity of an antigen presenting cell (APC). The second nucleic acid sequence is linked in frame to the first nucleic acid sequence or to a linker nucleic acid sequence and encodes an antigenic polypeptide or peptide. The methods and compositions of the present invention are useful as therapeutic vaccine for cancer and for major viral infections, such as hepatoma and cervical cancer, that cause morbidity and mortality. They can also be used in treating animal diseases, such as equine herpesvirus, bovine viruses, warek's diseases, retroviral and lentiviral diseases and rabies, in the veterinary medicine context. The present sequence represents the human papillomavirus (HPV) E7 antigenic protein
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Matches
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Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;
E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecule encoding a fusion polypeptide that promotes processing via the Major Histocompatibility Complex class I pathway and/or promotes activity of an antigen presenting cell, useful as vifor cancer and viral infections.
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                                                                                                 08-JAN-2003
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                                                               Modified HPV-E7
                                                                                                                                    ABB82376
                                                                                                                                                                    ABB82376 standard;
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                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQABPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
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                                                                                                 (first entry)
                                                               amino acid sequence
                                                                                                                                                                  protein;
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Pred. No. 7.6e-56;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid molecule that encodes a fusion CC polypeptide, comprising a first nucleic acid sequence encoding a comprise at least one immunogenicity-potentiating CC polypeptide, optionally, fused in frame with the nucleic acid, a linker comprise and that encodes an antigenic peptide or polypeptide. The nucleic acid encoding a linker peptide, and a nucleic acid that is linked comprise and that encodes an antigenic peptide or polypeptide. The nucleic acid molecule, polypeptides and vectors are useful as concines for enhancing immune responses, primarily cytotoxic Tector are completed (CTL) responses to specific antigens such as tumour or viral antigens, and for inhibiting growth or preventing re-growth of a tumour. The packaging cell line is useful for generating alphavirus replicon comparticles without contamination from replicon-competent virus. The pathogenic organisms include viruses such as human papilloma virus (HPV), hepatitis B virus, hepatitis C virus, human immunodeficiency virus, hepatitis B virus, and herpes simplex virus, intracellular parasites such as malaria, and bacteria that grow intracellular parasites such as malaria, and bacteria that grow intracellular parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-740856/80.
N-PSDB; ABV73162.
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                                                                                                                               chimeric
                                                                                                                                                                                       HPV-16 E7 protein SEQ ID NO:7.
                                                                                                                                                                                                                                                        29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                           ADE21865 standard; protein; 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or viral antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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                                                                                                                         fusion; translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                        (first entry
                                                                                              cancer;
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                                                                                                  tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 500; DB 5; Pred. No. 7.6e-56;
                                                                                           n; antigenic; cytostatic; HPV-16; E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                               immunotherapy;
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Human papillomavirus

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RESULT 99
ADO05276
ID ADO05
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AC ADO05
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DT 29-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a nucleic acid (I) encoding a chimeric CC fusion or fusion polypeptide, and a second domain comprising an antigen CC translocation polypeptide, and a second domain comprising an antigen CC having at least one antigenic peptide. Also described: (I) an expression CC vector comprising (I) operatively linked to a promoter and optionally, to CC one or more regulatory elements that enhance expression of the nucleic CC acid in a cell; (2) a particle comprising (I) or the expression vector; (CC acid in a cell; (2) a particle comprising (I) or the expression vector; (3) a cell that has been modified to comprising an antigen CC vector; (4) a chimeric polypeptide comprising an antigen an antigen polypeptide, and a second domain comprising an antigen CC comprising at least one antigenic peptide; (5) a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response, CC comprising (I), expression vector, particle, cell, cell of the particle, CC or the chimeric polypeptide; and a carrier or excipient; (6) inducing or enhancing an antigen specific immune response by administering the CC composition described above; (7) increasing the number of CDS + CTLs Specific for a selected desired antigen in a subject by administering the CC composition described above; and (8) inhibiting the growth of a tumour in a subject by administering the composition described above. (I) has CC composition described above; and can be used in immunotherapy, and gene therapy. The present sequence represents HPV-16 E7, which is used in the composition described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
major histocompatibility complex; MHC class I; vaccine; immune response;
                                                                                                                                                                             ADO05276 standard; protein; 99
                  Translocation domain;
                                                        Human papillomavirus type 16 E7 protein.
                                                                                                    29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding a chimeric fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain with an antigen having at least one antigenic peptide, useful for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 7; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.
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                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%;
96.9%;
                bacterial toxin; exotoxin A domain II; ETA;
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1.6e-56;
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ADU66377
ID ADU66377
ID ADU66377
AC ADU663
AC ADU663
XX
DT 10-FEB
XX
VACCIN
KW VACCIN
KW VACCIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid encoding a chimeric polypeptide comprising a translocation domain of a bacterial toxin and at least one antigenic peptide. The preferred translocation domain is domain II of Beudomonas aeruginosa exotoxin A (ETA(dII)) and the preferred antigen is antigen. The antigenic peptide comprises an epitope that binds to and is presented on the cell surface by major histocompatibility complex (MHC) class I proteins. The nucleic acid of the invention is useful as vaccine composition for enhancing antigen specific immune response, increasing the number of CDB+ cycotoxic T lymphocytes (CTLs) and for inhibiting the growth of a tumour. The present sequence is HPV-16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1999;
09-FEB-2000;
20-OCT-2000;
04-APR-2001;
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                             Human papillomavirus
                                                                                                                             10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 99
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N-PSDB; ADO05275.
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                                                         vaccine; MHC class I pathway;
E7 protein; E6 protein.
                                                                                                                                                         ADU66377;
                                                                                                                                                                                  ADU66377 standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; SEQ ID NO 7; 48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain II/human papilloma virus-16 E7 peptide useful for inducing or enhancing antigen specific immune response, or for inhibiting growth of tumor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 16.
                                                                                                Human papillomavirus type 16
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                                                                                                                                                                                                                                                                                                                                                                                   Local
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93; Conserv
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2000WO-US041422.
2001US-0281003P.
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Pred. No. 7.6e-56;
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                                                                                                   (HPV16)
                                                                      antigen
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                                                                                                E7 protein - SEQ
                                                                      specific
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                                                                       immune response;
                                                                                                                                                                                                                                                                                                                                                                                               Length 99;
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Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                               The invention comprises a nucleic acid molecule (DNA vaccine) that encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E7 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccine for inducing or enhancing immune response or for inhibiting or preventing tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu T,
                                                                                                                                                                                                                                                                                                  Sequence 99 AA;
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N-PSDB; ADU66361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 2; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-2003; 2003US-0467602P.
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                                                                           61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ 96
                                                                                                                                                                        1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                            l Similarity
93; Conservat
                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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ilarity 96.9%;
Conservative
                          2006, 05:10:00
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Match
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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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9-485-885-10

9-485-885-10

9-462-993-1

9-462-993-1

9-860-165-12

9-359-382-14

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US-10-011-749-24
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-011-749-46
US-10-980-523A-4
US-09-980-523A-10
US-09
 Sequence
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Sequence
Sequence
Sequence
Sequence
Sequence
 222, Appl
244, Appl
24, Appl
24, Appl
24, Appl
26, Appl
270, Appl
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US-09-980-523A-2

Sequence 2, Application US/09980523A

Patent No. 6783763

; GENERAL INFORMATION:
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                                                                        RESULT 2
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Patent No. 5679509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6126 ROCKY
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                      KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                          AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                               KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 158
                                                                                                                                                                                                   AVCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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6126 Rocky Way Court
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                                                                                                                                                                                                                                                                                                                                                                   Score 826; DB 1;
Pred. No. 8.2e-86;
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APPLICANT: BERHADD, HANS-ULRICH
APPLICANT: BERHADD, WALTER
APPLICANT: BERHADDE, WALTER
APPLICANT: BERHADDE, WALTER
APPLICANT: SIM, MUI MUI
APPLICANT: SIM, MUI MUI
TITLE OF INVENTION: THERAPPUTIC COMPOUNDS AND METHODS
FILE REFERENCE: BERN3001/JDB
CURRENT APPLICATION NUMBER: US/09/763,616
CURRENT APPLICATION NUMBER: PCT/AU99/00724
PRIOR APPLICATION NUMBER: PCT/AU99/00724
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: AU PO1645/99
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
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US-09-763-616-1
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                                                                                          US-09-763-616-1
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                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENCTH: 158
TYPE: PRT
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Patent No. 7019000
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE RUSE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEO ID NOS: 24
  Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADJ
APPLICANT: GUILLET, JEAN-GEE
APPLICANT: CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 158
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                            ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLD 120
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                    99.2%;
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Pred. No. 1.7e-85;
1; Mismatches 2; Indels
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Score 823; DB 3;
Pred. No. 1.7e-85;
1; Mismatches 2;
                                         Length 158;
    Indels
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US-08-316-239B-3
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                                                                                                                                                                                                                          Matches 148;
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: (703) 803-9387 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jagtiani, Ajay A. REGERRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/316,239B
FILLNG DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: C
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
     128
                                        121
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 158
                                      KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                          MFQDPQERPRKLPQLCTELQTT1HDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                         99.2%;
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Pred. No. 1.8e-85;
1; Mismatches 2; Indels
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CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
UNMBER OF SEQ ID NOS: 27
SOPTWARE: PATENTIN VOI: 2.0
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Description of Artificial Sequence: Gene US-08-860-165-10
US-09-359-382-10
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US-08-860-165-10
                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09359382

Patent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDMANDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

APPLICANT: GENER, Ian

APPLICANT: GENER, Ian

APPLICANT: GENER, Ian

APPLICANT: GENER, Ian

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 266
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
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                                            LENGTH: 26
TYPE: PRT
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EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
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CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
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                 ORGANISM: Human papillomavirus type
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ORGANISM: Artificial Sequence
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Pred. No. 3.2e-85;
1; Mismatches 2;
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Query Match

99.2%;

Score 823;

DB 2;

Length 266;

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APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
APPLICANT: MALLIAROS, JIM
ITITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 01727/0149
FULL REFERENCE: 01727/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Pacentin Ver. 2.1
SEQ ID NO 1
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US-09-367-309A-1
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US-09-485-885-4
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Patent No. 6342224
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                                              FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
                                                                                                                                APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, T
APPLICANT: Delisse, Anne-Ma
APPLICANT: Gerard, Catherin
                                                                                                APPLICANT: Lombardo-Benchei)
TITLE OF INVENTION: Vaccine
PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1998-08-17 PRIOR APPLICATION NUMBER: GB
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TYPE: PRT
ORGANISM: Human papillomavirus type 16
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                                                                                                                 Lombardo-Bencheikh, Angela
                                                                                                                                 Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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   GB 9717953.5
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Pred. No. 3.2e-85;
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     US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
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SOFTWARE: FRATSE
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORCANISM: Homo 8
US-09-485-885-10
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US-09-485-885-10
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows
SEQ ID NO 4
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Patent No. 6342224
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Best Local (
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                                                                                                                                                                                          Matches 148;
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TYPE: PRT
ORGANISM: Homo
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Best Local Similarity
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 23
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253
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pred. No. 3.6e-85;
1; Mismatches 2; Indels
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Pred. No. 3.3e-85;
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   283
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GENERAL INFORMATION:

Bruck, Claudine

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                                                                                                                                                             US-09-485-885-14
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                                                                                                    Query Match
Best Local
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SEQ ID NO 14
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APPLICANT:
APPLICANT:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOPTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                           LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                  Similarity
MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruck, Claudine
Bruck, Claudine
Cabezon Silva, Teresa
Celezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Angela
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                                                                                 Conservative
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                                                                                                  99.2%;
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Pred. No. 4.8e-85;
1; Mismatches 2
                                                                             Score 823; DB 2;
Pred. No. 5.1e-85;
1; Mismatches 2
                                                                             2;
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                                                                                                                Length 390
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APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PRO
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
FILE REFERENCE: N73477C GCW
CURRENT APPLICATION NUMBER: US/09/701,080C
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: GB 9811303.8
PRIOR APPLICATION NUMBER: GB 9811303.8
PRIOR FILING DATE: 1998-05-26
PRIOR PILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
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US-09-462-993-1
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US-09-701-080C-18
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; LENGTH: 151
; TYPE: PRT
                                                                                      SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6884786
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                                                                                                                           TITLE OF INVENTION: ANTITUWORAL COMPOSITION BASED ON IMMUNOC
TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
FILE REFERENCE: 017753-122
CURRENT APPLICATION NUMBER: US/09/462,993
CURRENT FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR APPLICATION NUMBER: P7/09152
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KIENY, Marie-Paule APPLICANT: BALLOUL, Jean-Marc APPLICANT: BIZOUARNE, Nadine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
ORGANISM: Artificial Sequence FEATURE:
                                          TYPE: PRT
                                                                   LENGTH:
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147; Conserv
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                                                                                                           PatentIn Ver. 2.2
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ilarity 97.4%;
Conservative
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Pred. No. 6.1e-85;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                  COMPOSITION BASED ON IMMUNOGENIC
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Sequence 12, Application US/08860165A

Sequence 12, Application US/08860165A

Patent No. 6004557

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
CURRENT APPLICATION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130

CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20

LENGER OF SEG ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEG ID NO 12

LENGER: 172
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PA
; FILE REFERENCE: 017227/0148
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US-09-359-382-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 172
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                               117 RHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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96.8%;
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94.7%; Pred. No. 2.5e-80;
tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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Pred. No. 5.7e-51;
                         PAPILLOMA VIRUS ANTIGENS
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: VARIBANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: PRT
CHARMSTANTISM. Artificial Sequence
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CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-14
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US-08-860-165-14
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LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08860165A Patent No. 6004557
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 RHLDKKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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96
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                                                                                                                                                                     Similarity
AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYN 93
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                                                                                                                                                    Conservative
                                                                                                                                                               57.6%;
92.5%;
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96.8%;
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Pred. No. 5.7e-51;
L; Mismatches 2
                                                                                                                                                                     Score 478; DB 2;
Pred. No. 2.6e-46;
                                                                                                                                                    Mismatches
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                                                                                                                                                                                       Length 172
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RESULT 17 US-09-359-382-14

Sequence 14, Application US/09359382 Patent No. 6306397

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US-08-117-083-10
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                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT TITORNEY/AGENT TITORNEY/AGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08117083 Patent No. 5719054
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SEQ ID NO 14
LENGTH: 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION UMBER: ECT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                        TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERRENCE/DOCKET NUMBER: A-58
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 017227/0148
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APPLICANT: FRAZER, Ian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 70
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                                                                                                        TELEFAX:
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ZIP: 94111
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San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walter H. Dreger
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Pred. No. 2.6e-46;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-247-904B-10
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Query Match 54.9%; Sometime Best Local Similarity 56.1%; Parameters 87; Conservative 21;
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APPLICANT: Rolfe,
APPLICANT: Eckste
                                                                                                                                                            TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/247
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKST NUMBER: MIV-
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
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                                                                                                                          LENGTH: 158 amino acids
TYPE: amino acid
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nes 97; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
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ZIP: 02109
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Eckstein, Jens W.
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the open reading frame."
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                                                                                                                                                                                                                                                         MIV-029.01
Score 455.5; DB 1;
Pred. No. 8.2e-44;
11; Mismatches 42;
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Pred. No. 3.6e-46;
Pred. No. 3.6e-46;
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                                 Length 158;
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US-08-767-942A-19
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; MOLECULE TYPE:
US-08-767-942A-19
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Best Local S
Matches 87
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOFTWARE: PATENTIAN PAPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                               LENGTH:
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                      KORPHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                              VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK 121
                                                                                                                       Application US/08767942A
                                                                                                                                           FODPOERPRKLPOLCTELOTTIHDIILECVYCKQOLLRREVYDFAFRDLCIVYRDGNPYA
 KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
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Berlin, Vivian
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                   54.9%; Score 455.5; DB 2; 56.1%; Pred. No. 8.2e-44;
                                                                                                                                                                                       21;
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                      Length 158;
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RESULT 21
US-08-117-083-14
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Patent No. 5
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/117,083
APPLICATION 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Boursnell, Michael E. APPLICANT: Inglis, Stephen C. APPLICANT: Munro, Alan J.
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                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
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                                                                                                                                                                                                                                                                                            LOCATION: 1..271
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
 125
                       122 KORFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
                                                                   65 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKDLNPAEKLHLNE 124
                                                                                      62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                            87;
                                                                                                                                      2 FODPOERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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KRRFHNIAGHYRGOCHSCCNRAROERLORRRETQV 159
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56.1%; Pred. No. 1.6e-43;
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the open reading frame."
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US-09-485-885-21

Sequence 21, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine

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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fas
SOFTWARE: Fas
SEQ ID NO 21
FONCTH: 278
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8 No. 634222
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APPLICANT: Cabezon &
APPLICANT: Delisse,
APPLICANT: Gerard,
APPLICANT: Lombardo-
TITLE OF INVENTION:
FILE REFERENCE: B45!
                                                                                                                                        Matches
                                                                                                                                                                             Query Match
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
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TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
ANT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
                                                           115 FEDPTRRPYKLPDLCTELNTSLQDIBITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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                                                                                                                                    ch 54.9%; Score 455.5; DB 2; Similarity 56.1%; Pred. No. 2.4e-43; 87; Conservative 21; Mismatches 42;
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VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                               FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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                                                                                                                                                                           Length 383;
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US-09-000-094-20
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                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-App-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WEBB,
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132 WTGRCMSC 139
                                     73 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                             72
                                                                                                                   13 IDOLCKTENLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG 72
                                                                                                                                                       12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                                 Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/AU96/00473 
*FILING DATE: 26-JUL-1996
                                                                         KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRRFHNIAGHYRGOCHSCCNRAROERLORRRETOV 269
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ZIP: 20007-5109
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WILLIAMS, Mark Philip
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                                                                                                                                                                                               36.6%; Score 304; DB 2; 39.8%; Pred. No. 3.4e-26; tive 29; Mismatches 48
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133 WKGRCLHC 140

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                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 51; Conserv
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Patent No. 6726912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WD PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE JOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WEBB, Elizabeth Ann
132 WTGRCMSC 139
                                                     73
                                                                            72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                               13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                       KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
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                                                                                                                                                                                                                                                                                                                                                         LENGTH: 368 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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39.8%; Pred. No. 3.4e-26;
ative 29; Mismatches 48
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-000-094-22
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US-09-000-094-22
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GENERAL INFORMATION:
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                    Query Match
Best Local :
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TELEFAX: (202) 672-5
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION NUMBER: WO PCT/AU96/00473
APPLICATION NUMBER: WO PCT/AU96/00473
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
AFTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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133 WKGRCLHC 140
                                  132 WIGRCMSC 139
                                                                                                                                                                                                                                  51;
                                                                                                                                                  13 IDQLCKTFNLSWHTLQINCVFCKNALTTABIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                         12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                         73 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                              72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                      Similarity
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COX, John Cooper
FRAZER, Ian
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WILLIAMS, Mark Philip
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                                                                                                                                                                                                                                                    Score 304; DB 2; Length 375; Pred. No. 3.5e-26;
                                                                                                                                                                                                                                    Mismatches
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US-09-000-094-24

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RESULT 27
US-10-011-749-22
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Patent No. 6726912
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                          Query Match 36.6%; Score 304; DB 2; Length 375; Best Local Similarity 39.8%; Pred. No. 3.5e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: ADVING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 11-Dec-2001
FILING DATE: 11-Dec-2001
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
133
                                      132 WTGRCMSC 139
                                                                                                                                                                   13
                                                                                  73
                                                                                                                                                                                                           12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
                                                                                                                                                                                                                                                   51;
WKGRCLHC 140
                                                                                KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                    KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                   IDQLCKTFNLSMHTLQINCVFCKNALTTABIYSYAYKHLKVLFRGGYPYAACACCLEFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 375 amino acids
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WILLIAMS, Mark Philip
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                                                                                                                                                                                                                                                     29; Mismatches
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RESULT 28

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RESULT 29
US-10-011-749-24
; Sequence 24, Application US/10011749
; Patent No. 6726912
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 51; Conserv
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TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-7UL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
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                                                                                                                               133 WKGRCLHC 140
                                                                                                                                                                       132 WTGRCMSC 139
                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                     72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                    13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                          12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                                               KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/000,094 FILING DATE: 21-Apr-1998 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09000094
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39.8%; Pred. No. 4.5e-26;
ative 29; Mismatches 48
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RESULT 30
US-09-000-094-46
; Sequence 46, Application US/09000094
; Patent No. 6365160
; GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 672-5:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WEBB
                                                                                                                                      133
                                                                                                                                                                         132 WTGRCMSC 139
                                                                                                                                                                                                                73 KINQYRHFDYAGYATTVEEETKODILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                             13 IDÓLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                  12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                                                                                     72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                      WKGRCLHC 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 465 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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MARGETTS, Mary Brigid
COX, John Cooper
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                                                                                                                                                                                                                                                                                                                                                                         36.6%; Score 304; DB 2; Length 465; 39.8%; Pred. No. 4.5e-26; tive 29; Mismatches 48; Indels
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US-10-011...
; Sequence 46, App...
; Patent No. 6725912
; Patent No. 6725912
; GENERAL INFORMATION:
; GENERAL INFORMATION: BLIZABETH Ann
MARGETTS, Mary Brigid
COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid;
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-000-094-46
                                                                                                                                                                  RESULT 31
US-10-011-749-46
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Best Local Similarity 39.8
Conservative
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TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,7
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDWARDS, Stirling John TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           699 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                 819 WKGRCLHC 826
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WILLIAMS, Mark Philip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 304; DB 2; Length 1587;
Pred. No. 2e-25;
19; Mismatches 48; Indels
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-011-749-46
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US-08-363-586-4
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                                                                                                               Sequence 4, Application US/08363586 Patent No. 5629161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of
TITLE OF INVENTION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 672-5:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    132 WTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                            699 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                                  759
                                                                                                                                                                                                                                                                                                                                                                                           72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                         WKGRCLHC 826
                                                                                                                                                                                                                                                                                                                                                  KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1587 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAZER, Ian
, Lutz
Use of HPV-16 E6 and E7-Gene Derived
Peptides for the Diagnostic Purpose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.6%; Score 304; DB 2; Length 1587; 39.8%; Pred. No. 2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
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US-09-980-523A-4
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                                                               PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.6%; Score 163; DB 1; Best Local Similarity 100.0%; Pred. No. 1.7e-11; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                    APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: FR 99/07012
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, II
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REGISTRATION NUMBER: 33,218
                         LENGTH: 30
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFQDPQERPRKLPQLCTELQTTIHDIILEC 30
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                                                                                                                                                                                                                                                                                                                      E6 AND E7
THEIR USE
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PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR PPLICATION NUMBER: FR 99/07012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 29
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                 APPLICANT: GISSMAN. Lutz
APPLICANT: MULLER, Martin
APPLICANTON: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR APPLICATION NUMBER: DE 199 05 883.0
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US-09-913-204-17
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US-09-913-204-17
                                                                                   NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6953579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOUNGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JASA-GERARD
APPLICANT: CONNAM, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT PEPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHOPPIN, JEANNINE APPLICANT: BOURGAULT VILLAD APPLICANT: GUILLET, JEAN-GE
                   ORGANISM: Bovine papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local

    Application US/09980523A
    6783763

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Similarity 96.6%;
28; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09913204
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100.0%; Pred. No. 1.7e-11;
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GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAN, FRANCINE

APPLICANT: CONNAN, FRANCINE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WOBL AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT APPLICATION NUMBER: PCT/FR00/01513

PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR APPLICATION NUMBER: FCT/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTMARE: Patentin Ver. 2.1
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US-09-601-729-276
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US-09-980-523A-10
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                                                                                                                                                                                                                                                                                                        APPLICANT: THIAM, KADER
APPLICANT: AURIAULT, CLL
APPLICANT: GRAS-MASSE, II
APPLICANT: LOING, ESTELL
APPLICANT: VERWAERDE, CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 10
LENGTH: 22
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Best Local Similarity 100.
Matches 22; Conservative
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 276
                                                                APPLICANT: AURIAUIT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: VERWAERDE, CLAUDIE
APPLICANT: VERWAERDE, CLAUDIE
APPLICANT: GUILLET, JEAN GERARD
APPLICANT: HOVENTION: LIPOPEPTIDES CONTAINING AN INTERPERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
TILE REFERENCE: USB-97-AU-IN
CURRENT FILING DATE: 2000-11-20
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/FR99/00259
PRIOR PILING DATE: 1999-02-05
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-02-06
                                            NUMBER OF SEQ ID NOS: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CPEEKORHLDKKORFHNIRGRW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LACVWCREPITEVDAFRCMIKDFHVVYRDGVKFGACTTCLE--NCLDKERRLWKGVPVTG 72
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GOULLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOOD AO IN.
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR PILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-03
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                                                                                 GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
                                                                                                                                                                                                                                                                                                                                                                               US-08-934-915-167
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LENGTH: 22
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100. Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                      Sequence 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide -09-601-729-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 23
         CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 RREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                                                                                                                                                                                                                                                  59324
CLEARWATER
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                                                                                                                                                                                                                                                                                                                                                      Application US/08934915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 124; DB 2; 100.0%; Pred. No. 3.1e-07;
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US-09-913-204-3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application Patent No. 6953579
GENERAL INFORMATION:
                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GISSMAN. Lutz
APPLICANT: MULLER, Herman
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134 PCUSO0
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             LENGTH: 137
TYPE: PRT
ORGANISM: Bovine papilloma virus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: LOUISE A. Foutch
                                                                                                                                            y Match 14.3%; Score 119; DB 2 Local Similarity 28.9%; Pred. No. 1e-05; hes 35; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 PILING DATE: 22-SEP-1997
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les 21; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 RWTGRCMSCCRSSRTRRETQL 151
88 LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR-WTGRCMSCCR-SSRT 145
                                                                15 LDCLWCREPLTEVDAFRCMVKDFHVVIREGCRYGACTICLENCLATERRLWQGVPVTGEE 74
                                                                                                       28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
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100.0%; Pred. No. 8.2e-(
ive 0; Mismatches
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US-09-913-204-7
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; ORGANISM: Bovine papilloma virus US-09-913-204-13
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                                         SEQ ID NO 13
LENGTH: 137
TYPE: PRT
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PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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Patent No. 6953579
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APPLICANT: MULLER, Martin
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134PCUS09
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                   APPLICANT: MUILER, MARTIN
APPLICANT: MUILER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSONERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
                                                                                                   PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
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5. 6953579
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                                                                                                           US-08-934-915-166
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Patent No. 59324
GENERAL INFORMA
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Best Local Similarity
                                          Matches
                                                                         Query Match
                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHENG, HWE
TITLE OF INVENTION: S
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3.0 SOFTWARE: Microsoft word 6.0 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                           MOLECULE TYPE:
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                                                                                                                                       LENGTH: 21 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 22-SEP-1997
                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
115 KQRHLDKKQRFHNIRGRWTGR 135
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o. 5932412
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                                                        13.9%;
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28.9%; Pred. No. 1e-05;
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
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                                                                                                                                                                                                                                                                                                                                                                             07/949,836
                                                                                                                                                                                                                                                                                         1946.6
                                          ۲.
                                                          Score 115; DB 1
Pred. No. 3e-06;
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                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF HUMAN
                                                                           DB 1; Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500
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                                            Indels
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                                            0;
                                            Gaps
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RESULT 45
US-08-164-768-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-UNU-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
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                                                                                                                                                                                                     Query Match
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,953

PILING DATE: 08-MAY-1991

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 40 15 044.5

FILING DATE: 10-MAY-1990

CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bleul, Conrad
APPLICANT: Gissmann, Lutz
APPLICANT: Muller, Martin
TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of
TITLE OF INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Manspeizer, David A.
REGISTRATION NUMBER: 37,540
REFERENCE/DOCKET NUMBER: 05552.1075-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/947,992 FILING DATE: 21-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                              h 13.9%;
Similarity 64.5%;
                                                                                                                      DPQERPRKLPQLCTELQTTIHDIILECVYCK 34
                                                                             DPTRRPYKLPDLCTELNTSLQDIEITCVYCK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08466285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                   (202)408-4400
(202)408-4400
TN NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                Score 115; DB 1
Pred. No. 5e-06;
                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                     DB 1; Length 32;
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                                                                                                                                                            0,
                                                                                                                                                            Gaps
                                                                                                                                                            0;
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RESULT 46
US-09-601-729-278

// MOLECULE TYPE: peptide
US-08-164-768-2
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TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 278, App
Patent No. 668305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08164768 Patent No. 6322794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                APPLICANT: GUILLET, JEAN GERARD
TITLE OF INVENTION: LIFOPEPFIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: US/09/601,729
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/FR99/00259
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                       APPLICANT: THIAM, KADER
APPLICANT: AURIAULT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: VERWAERDE, CLAUDIE
PRIOR APPLICATION NUMBER: 98 01439
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FCTORS DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FORMAN, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1300
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPÉLICANT: GISSMÂNN, Lutz
APPLICANT: MULLER, MAITLIN
TITLE OP INVENTION: SEROREACTIVE EPITOPES
TITLE OP INVENTION: HUMAN PAPILLOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & ADDRESSEE: DUNNER, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               un 13.9%;
1 Similarity 64.5%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPTRRPYKLPDLCTELNTSLQDIBITCVYCK 31
                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09601729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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Pred. No. 5e-06;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON PROTEINS OF (HPV) 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
TITLE OF INVENTION: Associated Cancers
FILE REFERENCE: 3352-2-2
CURRENT APPLICATION NUMBER: US/10/612/818
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR APPLICATION NUMBER: US 99/828,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 22
Type: Dem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence; FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-09-601-729-278
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US-08-934-915-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 278
LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10612818 Patent No. 6933123
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Best Local Similarity
                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                        GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: CHENG, HWEE-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAI

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Derived from the E6 early coding region of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                    NUMBER OF SEQUENCES: 1
                 ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 EKQRHLDKKQRFHNIRGRWT 133
                                                                                                                                                                                                                                                                                  44,
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                                                                                                                                                                                                                                                                4, Application US/08934915
5932412
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CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                            RDGNPYAVCDKCLKFYSKISEY 22
                                                                                                                                                                                                                                                                                                                                                                                                               RDGNPYAVXDKCLKFYSKISEY 76
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ilarity 100.0%; Pred. No. 3.
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 114; DB 2; 95.5%; Pred. No. 4.2e-06;
                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                    OF HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 49
US-08-934-915-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOTTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TYPE: lamino acid
TOPOLOGY: linear
                                                                                                                                                                      COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: MICROSOft WORD 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                        APPLICATION NUMBER: US
FILING DATE: 22-SEP-15
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHEFIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMPUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & A
                  ATTORNEY/AGENT INFORMATION: NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                       STATE: F
                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
NAME: LOUISE A. Foutch REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 YSKISEYRHYCYSVYGTTLE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSKISEYRHYCYSLYGTTLE
                                                                                                                                                                                                                                                                                                                FLORIDA
                                                                                                                                                                                                                                                                                                                                                  E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       813-538-3820
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                                                                                                                       22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%;
                                                                               07/949,836
  37,133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109; DB 1; Length 20; Pred. No. 1.4e-05;
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; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 50
US-08-934-915-163
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
    Query Match 13.1%;
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 163, Application US/08934915 Patent No. 5932412
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                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DILLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN IMPUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMPUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 813-538-3800 TELEPAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: F
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CITY: CLEARWATER
                                                                                                                                                                                                                                                TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1946.6
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 13.1%; Score 109; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 1.4e-05; es 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLORIDA
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17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILLNER, JOAKIM
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                                                                                                                                                                                                                                                                                                                                                                                                               07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/934,915
                                                                                                                                                                                                                                                                                                                          37,133
  Score 109; DB 1; Length 20; Pred. No. 1.4e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            1946.6
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    Gaps
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Sequence 165, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
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RESULT 52
US-08-934-915-165
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                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 164, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILLING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LILLING APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE
CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                          85 GTTLEQQYNKPLCDLLIRCI 104
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                                                                                                                                                        Conservative
                                                                                                                                                                        12.5%;
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                                                                                                                                                      1; Mismatches
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                                                                                                                                                                        Score 104; DB 1;
Pred. No. 5.1e-05;
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                                                                                                                                                                                            Length 20;
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0,

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:

11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES

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RESULT 53
US-08-934-915-159
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8, TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56, TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR TITLE OF INVENTION: DIAGNOSTIC PURPOSES NUMBER OF SEQUENCES: 193
CORRESSEE: MASON & ASSOCIATES, P.A. STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,9:
FILING DATE: 22-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/949,836
APPLICATION NUMBER: 07/949,836
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: MICTOSOFT WORD 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA APPLICANT: CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: CLEARWATER STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 813-538-3820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159, Application US/08934915
5. 5932412
                                                                                                                                                  FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%; Score 104; DB 1; ilarity 95.0%; Pred. No. 5.1e-05; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/934,915
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                                                                                                                                                                                                                                                                                                                                                                 OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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GENERAL INFORMATION:

APPLICANT: DILLMER, JOAKIM

APPLICANT: DILLMER, LENA

APPLICANT: CHENG, HWEE-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIBUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193
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US-08-934-915-160
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,9:

FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEPAX: 813-538-3820
                                                                           FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                           813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%;
95.0%;
                                                                                                                                                                                                                                                                                                US/08/934,915
                                                                                                                                                                                                                  07/949,836
                                                                                                                                     37,133
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                      160:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1946.6
                                                                                                                      1946.6
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Pred. No. 0.00024
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US-08-934-915-161
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                                                                                                                          ; MOLECULE TYPE: peptide US-08-934-915-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                             Query Match
Best Local 9
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                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,13:
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEB: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 17757 U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                           Local Similarity
nes 17; Conserv
                                                                                                                                                        LENGTH: 20 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                      TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 11.7%;
Local Similarity 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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              REVYDFAFRDLCIVYRDGNP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLORIDA
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                                                           11.7%;
llarity 85.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1997
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Pred. No. 0.00031
                                                           Score 97; DB 1; Le
Pred. No. 0.00031;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 20,
                                                                                         DB 1; Length 20;
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                                                             Gaps
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RESULT 56

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STATE:
COUNTRY: USA
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/466,768
FILING DATE: 10-DEC-993
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/947,992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 46524
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Applic
Patent No. 5753233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.3%; Score 94; DB 3; Lobest Local Similarity 100.0%; Pred. No. 0.00049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bleul, Conrad
APPLICANT: Gissmann, Lutz
APPLICANT: Miler, Martin
TITLE OF INVENTION: Seroreactive Epitopes On Proteins
TITLE OF INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabo
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 FHNIRGRWIGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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US-08-164-768-4
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                           TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08164768 Patent No. 6322794
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                                                                                                                               APPLICATION UNMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FORMAN, DAVId S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552.1075-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-44000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202)408-400
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BLEUL, Conrad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Manapelzer, David A.
REGISTRATION NUMBER: 37,540
REFERENCE/DOCKET NUMBER: 05552.1075-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GISSMANN, Lutz
APPLICANT: MULLER, MARTIN
TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: 10-MAY-1
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT ADDRESSEE: DUNNER, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 08-MAY-1991 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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single
linear
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Pred. No. 0.0016;
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US-09-641-528B-46535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 60
US-08-934-915-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46535
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, Applica Patent No. 5932412 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46535, Application US/09641528B Patent No. 7026443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celia, Esteban
APPLICANT: Celia, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REPERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
STATE: U.S.A.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          APPLICANT: DILLMER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                               ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 11.1%; Score 92; DB Local Similarity 100.0%; Pred. No. 0.0 tes 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 RGRWTGRCMSCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGRWTGRCMSCCRSS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08934915
                                                                                                                                                                                                                                                                                                                                                    DILLNER, JOAKIM
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Pred. No. 0.0016;
3; Mismatches
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o. 0.00082;
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US-08-363-586-3
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                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC comparable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHOLINI PC-DOS/MS-DOS
SOFTWARE: PACHOLINI PC-DOS/MS-DOS
SOFTWARE: PACHOLINI PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1991
APPLICATION UNUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: WESTICH INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08363586 Patent No. 5629161
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APPLICANT: Muelle
APPLICANT: Gissma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION UNMER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECONMUNICATION INFORMATION:
TELEPHAX: 813-538-3800
TELEPAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ring
ADDRESSEE: Dunner
ADDRESSEE: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
OLECTRO
                                   NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Use of HPV-16 E6
TITLE OF INVENTION: Peptides for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
TELEPHONE: 202-/
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                      202-408-4000
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                                                                   33,218
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Pred. No. 0.0012;
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Diagnostic Purpose
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FILE REFERENCE: 2060.0100001

CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR FILING DATE: 1999-12-10

NUMBER OF EQ ID NOS: 51505

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 46517

LENGTH: 15

TYPE: PRT
                                                                                                                  ; Sequence 2, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALEFSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC PEPTITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CTITY: Pall Alto
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US-07-909-122-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 702644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Cells, Esteban
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                       COUNTRY: USA
ZIP: 94304-1018
                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 10.8%; S
Local Similarity 100.0%; les 16; Conservative 0;
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                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                          California
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                                                                                                                                                                                                                    DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 89; 100.0%; Pred. No.
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Pred. No.
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0.0018;
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1090-11-10
NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46523
LENGTH: 15
RESULT 65

US-09-641-528B-46525

; Sequence 46525, Application US/09641528B

; Patent No. 7026443

; GENERAL INFORMATION:
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REGISTRATION NUMBER: 25,952
REFERENCE/DOCKET NUMBER: 28600-20105.01
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                        10.2%; Score 85; 100.0%; Pred. No.
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                                                                                                                                                                                                                                           DB 3; 1
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    US-09-641-528B-51200
; Sequence 51200, Application US/09641528B
; Patent No. 7026443
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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46525
밁
                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46526
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APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 5105
SOCTUARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46525
LENGTH: 15
                                                                                                                                                                                                                                                                                                               APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Cory, Howard
TITLE OF INVENTION: INDICING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51905
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
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                                                                                                             Query Match
Best Local (
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                                                                                            Matches
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                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 15; Conserva
                                                                                                             Match 10.2%;
Local Similarity 93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GRCMSCCRSSRTRRE 148
                             78 HYCYSVYGTTLEQQY 92
                                                                                            14;
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  HYCYSLYGTTLEQQY
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                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>.
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                                                                                                               Score 85; DB 3; Length 15; Pred. No. 0.0051;
                                                                                            Mismatches
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                                                                                              Indels
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                                                                                              Gaps
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RESULT 69
US-09-641-528B-46534
; Sequence 46534, Application US/09641528B
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Best Local Similarity
Matches 15; Conserv
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TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51200
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Ceils, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
PILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
CURRENT FILING DATE: 2000-08-15
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sette, Alessandro APPLICANT: Sidney, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                       44 DFAFRDLCIVYRDGN 58
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Celis, Esteban
Grey, Howard
                                                                                                   DFAFRDLCIVYRDGN 15
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                   10.1%; Score 84;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 85;
100.0%; Pred. No.
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0.0067;
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0.0051;
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Gray, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: US 60/172,705
FRIOR APPLICATION NUMBER: US 60/172,705
FRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46522
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                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46522
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US-09-641-528B-46522
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Grey, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,5288
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR TILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46534
LENGTH: 15
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                                                                                Matches
                                                                                                                          Query Match
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                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                          TYPE:
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                                          29 ECVYCKQQLLRREVY 43
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                                                                                  l Similarity
15; Conservat
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Southwood, Scott
Chesnut, Robert
Celis, Esteban
Grey, Howard
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ECVYCKOQLLRREVY 15
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                                                                                  Conservative
                                                                         100.08; --
                                                                                                      10.0%; Score 83; DB 3; 100.0%; Pred. No. 0.0086;
                                                                                  Mismatches
                                                                                                                          Length 15;
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                                                                                  Indels
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                                                                                  Gaps
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RESULT 71 US-09-641-528B-46527

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US-09-641-528B-46536
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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46527
밁
                                                                                                                                                          US-09-641-528B-46536
                                                                                                                                                                                                                                             APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0 46527
                                                                                               Query Match
Best Local :
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                                                                             Matches
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CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
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APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
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                                                                                                                                                                            OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                   42 VYDFAFRDLCIVYRD 56
                                                                                               Similarity
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Southwood, Scours
Thranut, Robert
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                                                                             Conservative
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                                                                                             100.0%;
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Pred. No.
                                                                                             Score 83;
Pred. No.
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                                                                             Mismatches
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0.0086;
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0.0086;
                                                                                                                Length 15
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RESULT 73

REFERENCE/DOCKET NUMBER:

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TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER: OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50556
LENGTH: 15
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                               COUNTRY: USA
COUNTRY: USA
2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/075,541D
FILING DATE: 10-UN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
ANACE: ALAN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
NAME: NADEL, ALAN S REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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Grey, Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08075541D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chesnut,
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1601 MARKET STREET, 36TH FLOOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09641528B
                     ALAN S
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US-09-641-528B-51199
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                          Sequence 51250, Application US/09641528B
Patent NO. 7026443
Patent NO. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: UNING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TITLE DEFERENCE, 2060 100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Crey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT PELICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US/60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 51199
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
CURRENT APPLICATION NUMBER: US/09/641,528B
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                 2060.0100001
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Pred.
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RESULT 78
US-09-641-528B-46518
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US-09-270-767-41452
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT EPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41422
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PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR, FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 51250
LENGTH: 15
                                                                                                                                                                                                        Sequence 46518, Application US/09641528B Patent No. 7026443 GENERAL INFORMATION:
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Clis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
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OTHER INFORMATION: Xaa means any amino acid
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Local Similarity 93.3%;
les 14; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 -----AVXDKCLKFYSKISEYRHY----CYSVYGTT-LEQQYNKPLC-----
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Pred. No. 0.011;
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US-09-641-528B-47291
US-09-641-528B-47291; Application US/09641528B; Sequence 47291, Application US/09641528B; Patent No. 7026443; GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Grey, Howard
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APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
APPLICANT: Grey, Howard
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51905
SOPTWARE: FASTSEQ for Windows Version 4.0
LENGTH-15
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Best Local Similarity 93...
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46520, Application US/09641528B Patent No. 7026443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sette, Alessandro
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Peptide Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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100.0%; Pred. No. 0.019;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Human Papillomavirus
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0.015;
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RESULT 82
US-09-641-528B-46532
; Sequence 46532, Application US/09641528B
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Best Local Similarity
Watches 12; Conserve
             GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
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US-09-641-528B-50558
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APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Grey, Howard
APPLICANT: Grey, Howard
APPLICANT: Grey, Howard
APPLICANT: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1909-12-10
NUMBER OF SEQ ID NOS: 51505
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50558
LENGTH: 15
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CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
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NT: Chesnut, Robert
NT: Celis, Esteban
NT: Grey, Howard
F INVENTION: INDUCING C
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15; Conserv
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Pred. No.
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0.019;
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CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS

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FILE REFERENCE: 2060.0100001

CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 51505

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 46532

LENGTH: 15
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US-09-641-528B-46516
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                                                                                               Sequence 46528, Application US/09641528B Patent No. 7026443 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46516
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Best Local Similarity
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APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
FILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
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                                                                                                                                                                                                                                                                                                                                                              -09-641-528B-46516
                                             APPLICANT: Sette, Alessandro APPLICANT: Sidney, John APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/641,528B
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                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/172,705 PRIOR FILING DATE: 1999-12-10
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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5. 7026443
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         Southwood, Scott
Chesnut, Robert
Celis, Esteban
                                                                                                                                                                                                                       CIVYRDGNPYAVCDK 15
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Southwood, Scott
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                                                                                                                                                                                                                                                                                                      9.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                        DB 3;
0.032;
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0.025;
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RESULT 86
US-09-270-767-46957
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Best Local S
Matches 14
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TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31740
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CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 51505

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 46528
                                                                                                                                              Sequence 46957, Appl Patent No. 6703491 GENERAL INFORMATION:
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                     CTSFHYFPRLNENGKKLLLPCDFCDVNFEFAHDFLAHSEEKHLNKKKREKETRNTGAGRI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                        Application US/09270767
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PRICING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASCEQ for Windows Version 4.0
SEQ ID NO 6366
LENGTH: 572
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US-09-949-016-6366
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US-09-641-528B-46521

US-09-641-528B-46521; Application US/09641528B; Patent No. 7026443
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Best Local Similarity 22.4%; Pred. No. 2.8;
Matches 41; Conservative 21; Mismatches
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ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                88 -LEQQYNKPLC-----DLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC 136
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US-09-641-520B-50557

US-09-641-520B-50557, Application US/09641528B

; Sequence 50557, Application US/09641528B

; Patent No. 7026443
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                                                                                                                                                ; OTHER INFORMATION: Peptide Derived from US-09-641-528B-50557
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TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46521
LENGTH: 15
                                                                                                                                                                                                                                       TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PAPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER: OF SEO ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50557
LENGTH: 15
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Best Local Similarity 93.3%;
Matches 14; Conservative
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APPLICANT: Sette, Alessandro
                                                                         Matches
                                                                                           Query Match
Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                               TYPE: PRT
                       50 LCIVYRDGNPYAVXD
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                                                                         14;
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Celis, Esteban
Grey, Howard
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LCIVYRDGNPYAVCD
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Chesnut, Robert
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Pred. No.
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Pred. No.
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RESULT 90 US-09-641-528B-50559 ; Sequence 50559, Application US/09641528B

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TITLE OF INVENTION: No. 6989232el Proteins an
FILE REFERENCE: 21402-099
CURRENT APPLICATION UNMBER: US/09/939,853A
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/228,191
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/267,300
PRIOR FILING DATE: 2001-02-08
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US-09-641-528B-50559
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 159
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
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Best Local S
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 50559
LENGTH: 15
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Best Local :
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APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celia, Esteban
APPLICANT: Celia, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REPERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/05/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR PILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 698923
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/269,961
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/277,337
PRIOR FILING DATE: 2001-03-20
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APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 785
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133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 QQLLRREVYDFAFRD 49
                                                                                                                                                                         16 CTELQ-TTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK-FYSKI 73
                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                   SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRW- 132
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-TGRCMSCC 140
                                                                                                                               CTEAEGRTWHMKHFACQECEHQLGGQR-----YIMREGKPY----CLACFDTMF 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09939853A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 77; DB 3; Length 15; ilarity 100.0%; Pred. No. 0.041; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              John
                                                                                                                                                                                                                                         9.2%; Score 76.5; D
24.0%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6989232el Proteins and Nucleic Acids Encoding
                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                              DB 2; Length 785;
                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                       Indels
                                         ----VDQGQMSHDGQ-HWH 391
                                                                                                                                                                                                                  53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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RESULT 93
US-09-641-528B-46529
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US-07-909-122-4
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                                                                                                                                                                                                                                                   Sequence 46529, Application US/09641528B Patent No. 7026443
GENERAL INFORMATION:
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Patent No. 5415995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION GYSTEM: PC-DOS/MS-DOS
OPERATION GYSTEM: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REFERENCE/DOCKET NUMBER: 28600-2010:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SCHOOL
APPLICANT: PALEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 9.2%; Score 76;
Local Similarity 100.0%; Pred. No.
19: 14; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                         1 LRREVYDFAFRDLC 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALEFSKY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIRUS
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0.05;
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Sequence 16235, Application US/09248796A

Patent NO. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO (
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
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US-09-641-528B-46531
; Sequence 46531, Application US/09641528B
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US-09-248-796A-16235
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CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR FILING DATE: 1999-12-10

NUMBER OF SEQ ID NOS: 51505

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 46531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46529
LENGTH: 15
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GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conser
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SEQ ID NO 16235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USUNG PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sette, Alessandro APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   93 NKPLCDLLIRCINXQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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100.0%; Pred. No.
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Pred. No. 0.054;
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0.054;
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RESULT 96
US-09-949-016-8090
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US-09-949-016-8090
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: USING PEP
                                                                                                                                                                                                                                                           RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8090
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR ADD: TOWNSTANDERS 105/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.1%;
Best Local Similarity 22.9%;
Matches 33; Conservative 1
                                                                                                                                                                           GENERAL INFORMATION:
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Best Local :
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TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 RDGNPYAVXDKCLKFYS-KISEYRH----YCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 RICNHRDTYHHHPYTCHHIFCLCICHGIYCHPCNDHVFACHHIFCHCIYHGTYRHPCICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 QLCTELQT-----TIHDIILEC----VYCK------QQLLRREVYDFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 --GTYYPIYHRISYLCSDRLCVCHHTCPCICHPIYRDTSYLCIYRPICHLSIYCRHHQ-- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                           66 GLCDLYPCCLCDYKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-KTTNRILASSCCSSN
                                                                                                                                                                                                                                                                                                                                                                 95 PLCDLLIRCINXOKPLCPEEKORHL------DKKORFHNIRGRWTGRCM--SCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                              26 RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCPEEKORH-----LDKKORFHNI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%;
nilarity 27.5%;
Conservative 1
  INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75.5; Di
; Pred. No. 1.2;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75.5; D
Pred. No. 1.8;
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FILE REFERENCE: 2060.0100001

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US-09-186-723-7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-377-309-7
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US-08-377-309-7
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GENERAL INFORMATION:
APPLICANT: MAIGHA.
RECOMBINANT HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005002
CURRENT APPLICATION NUMBER: US/09/186,723
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 08/377,309
EARLIER APPLICATION NUMBER: 08/377,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Murgita, Robert A.
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005001
CURRENT APPLICATION UNMERR: US/08/377,309A
CURRENT FILING DATE: 1995-01-24
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LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                       Sequence 7, Application US/09186723 Patent No. 6288034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.0%; Score 74.5; DB 1; Length 393; Best Local Similarity 23.4%; Pred. No. 3.9; Matches 34; Conservative 26; Mismatches 44; Indels 4
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Patent No. 5965528
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Best Local (
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PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                  169
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Pred. No.
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RESULT 100
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,012
FILING DATE: 21-ULL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNUMBER: US 08/377,317
FILING DATE: 24-DAN-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 06727/007001
TELEPANCE/DOCKET NUMBER: 06727/007001
TELEPANCE: (617) 542-8906
TELEPAN: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08505012 Patent No. 6331611
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Best Local Similarity 23.4%;
Query Match 9.0%;
Best Local Similarity 23.4%;
Matches 34; Conservative 26
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
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APPLICANT: Murgit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Murgita, Rol
TITLE OF INVENTION: EXI
TITLE OF INVENTION: HOW
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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MEDIUM TYPE: Floppy disk
                                                                                   MOLECULE TYPE: protein
                                                                                                                   TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert A.
 26;
 Score 74.5; DI
Pred. No. 3.9;
26; Mismatches
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Pred. No. 3.9;
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Suite 3100
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  of hits satisfying
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3: geneseqp2000s:*
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5: geneseqp2002s:*
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Gapop 10.0
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Match
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196.288 Million cell updates/sec
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   chosen parameters:
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ADO22640

AAO22636

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AAO22636

AAO24072

AAW35742

AAW357466

AAW22766

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Ado22636 HPV prote
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Ado44072 Amino aci
Adw35742 Human pap
Ado44660 Amino aci
Adw66364 Human pap
Ado426262 Human pap
Ado636363 Human pap
Ado6363 Human pap
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Ade40817 Anti-apop
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AEF40157
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AAR277253
AAR2752634
AAY225376
AAY22537
AAX253837
                                                                                                                                                                                                                                                                              Aed52634 Fusion pr

Aay25379 HPV fusion

Aay02635 Pusion pr

Aed52642 Fusion pr

Aay25377 HPV fusion

Aay02637 Brott D1/3

Aed52638 Fusion pr

Aay25381 HPV fusion

Aay02637 CLYTA-E6E

Aed52646 Fusion pr

Aed44066 Amino aci

Aay57808 HPV-10 E6

Ad190078 Human pap

Aaw99369 Papilloma

Aar40911 HPV E6 re

Ad044077 Amino aci

Aea9853 HPV (onco

Aec98865 HPV 31 En

Aec98865 HPV prote

Aab98434 Human pap

Aab98434 Human pap

Aab98437 HPV (onco

Aec98868 HPV 31 En

Aec98868 HPV Jonco

Aec98868 HPV 58 En

Aea98536 HPV [onco

Aec98870 HPV [onco

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Aay25376 HPV fusio
Aay02632 Prot. D1/3
Aed52634 Fusion pr
Aay02635 CLYTA-E6-
Aay02635 CLYTA-E6-
Aed52642 Fusion pr
Aay02637 Frot D1/3
Aed52638 Fusion pr
Aay02637 CLYTA-E66
Aay0267 CLYTA-E66
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Adr47005 Human pa
Aef40157 Human pa
Aar27725 HPV 16
Aar277561 Human pa
   Aay25386
Aay02642
Aed52657
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                                                                                                                                                                     protein is designated E677etM, and comprises an E6 amino terminus (where residues 63 and 106 have been replaced with glycine) and an E7 carboxy terminus (where residues 24 and 26 have been replaced with glycine). E687TetM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
Query Match
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Matches 149
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                                                                                                                       Sequence 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a fusion protein, comprising E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60

Local Similarity

149;

Conservative

<u>,</u>

Length 248; Indels

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Gaps

0

Best Local Similarity

99.8%; 98.7%;

Score Pred.

828; DB 8; No. 4.6e-84;

Length 248

Query Match

Sequence 248

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cc polypeptides from human papillomavirus type 16 (HPV16). The fusion comprising E6 and E7 crowner in is designated E6E7PentM, and comprises an E6 amino terminus cc (where residues 63 and 106 have been replaced with glycine) and an E7 carboxy terminus (where residues 24, 26 and 91 have been replaced with CC glycine). E6E7PentM is representative of fusion proteins of the cc invention. The specification describes human papillomavirus E6 and E7 cc polypeptides, where the E7 polypeptide has mutations at any one or more cf the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has caids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating conditionation treating the fusion proteins are useful for generating conditionation treating the fusion proteins are useful for generating conditionation treating the fusion proteins are useful for generating conditionation treating the fusion proteins are useful for generating conditionation treating the fusion proteins are useful for generating conditionation treating treating the reproductive system, including penile and vulvar cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 70-71; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
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N-PSDB; ADO44065.
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MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY	Score 826; DE Pred. No. 4.2e ; Mismatches		inven	E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence	eing i	(pre-)	e tor	r E7 p	on or	growth	method fo	al i ch	tide a	Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incub		en M;								therapy;	27.					RETOL	AVGDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINGQKPLCPEEKQRHLD	TLEQQYI	MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY	ILECVY	Mismatches
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REVYDE	Length 151			preven	with	one gro	mediat	of HPV	the c	atient	rminin		cting), com										CT .							LIRCIN	LIRCIN	REVYDE	REVYDE	Indels
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Best Local S
Matches 149
                                                                                                                                                                                   The invention relates to a novel method for determining the possibility of recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV) or suspected of being infected with HPV, and has or had a (pre-)cancerous growth on or around the cervix. The novel method comprises incubating an E6 or E7 peptide of HPV with a sample from the patient, and assaying the sample for a cell-mediated immune response against the peptide. The method is useful for determining the possibility and preventing the recurrence of a (pre-)cancerous growth in a patient infected with HPV or suspected of being infected with HPV. The HPV E6 or E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incubating the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth; cancer; human papilloma virus; cervix; cell-mediated immune response; HPV; HPV-16.
                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 125-126; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sastry KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2001; 2001US-0306809P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
99.5%;
nilarity 98.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tortolero-Luna G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID No
Score 826; DB 6;
Pred. No. 4.2e-84;
0; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Follen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                Length 151;
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RESULT 5
AD0440772
ID AD04
AC CAP
AC AD04
AC A
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                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a wild type E6 protein from human papillomavirus type 16 (HPV16), which is used to produce fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and mucleic acids encoding the fusion proteins are useful for generating jamunue responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for treating or prevent cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 76-77; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-316328/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002; 2002US-0415929P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004
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                                                                                                                                                                                                                                                       149;
61
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                                                                                                                                                                                                                                                                                     Similarity
                              AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
AVCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                      MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY 60
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                              99.5%;
98.7%;
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                                                                                                                                                                                                                                                Score 826; DB 8;
Pred. No. 4.2e-84;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                            Length 151;
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RESULT 6
AAW35742
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                                                                                             Methods have been developed for distinguishing a subset of human CC papilloma virus (HPV) that is associated with an increased risk of C papilloma virus (HPV) that is associated with an increased risk of CC papilloma virus (HPV) that is associated with an increased risk of CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the CC sample and determining if the base at position 350 of the E6 gene (see CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of GC at position 350 is associated with an increased risk of developing CC cervical dysplasia or cervical cancer; and (2) preparing a cervical sample to expose any HPV-16 E6 protein in the sample and determining if the amino acid at position 83 of the protein (see position 90 in AAW35741 and AAW35742 for comparison) is Val or Leu, where the presence of Val at CC position 83 that is associated with an increased risk of developing CC cervical dysplasia or cervical cancer. The present sequence represents the variant protein sequence for HPV-16 E6. The 350G variant correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4 CC in negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III; CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
              Query Match
Best Local Similarity
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evaluating risk of cervical dysplasia or cervical cancer - variant form of human papilloma virus 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT94742.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Col 23-26; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5679509-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome; circular; human papillomavirus type 16; HPV16 E6; cervical dysplasia; cervical cancer; cervical smear.
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16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW35742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-525714/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheeler CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 16 E6 protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW35742 standard; protein; 162
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                                                                  162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parmenter
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(first entry)
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residues are given following on"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Mutated from Leu in the reference (AAW35741)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
              99.5%;
Score 826; DB 2;
Pred. No. 4.6e-84;
0; Mismatches 2
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                              Length 162;
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Conservative

<u>,,</u>

Indels

0

Gaps

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RESULT 7
AD044060
ID AD044060
AC AD04
XX AD04
XX AD04
XX AD04
XX B6 F
D7 15-1
XX B6 F
WW Cerr
WW Cerr
WW anal
XX W AD02
XX Huma
OS Synth
XX WO20
XX IS F
PD 15-P
XX WO20
XX WAD1
PR 03-C
PR 03-C
PR N-PS
XX New
PT usef
PT cann
XX New
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PT cann
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XX New
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PT cann
XX One
CC The
CC Whell
CC Whell
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CC Usel
CC Conc
CC Genc
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                              Query Match
Best Local Similarity
                                                                                                                                                                             The present sequence represents an E6E7 fusion protein, comprising wild type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 67-68; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-316328/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004
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                                                                                                                           Sequence 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anal cancer; reproductive system cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of an E6E7 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassetti MC;
                                                                                                                           AA;
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                          99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
Score 826; DB 8;
Pred. No. 7.7e-84;
0; Mismatches 2
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                                                            Length 248;
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                                                                                                               Matches 148;
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                             The invention comprises a nucleic acid molecule (DNA vaccine) that encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E6 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccin for inducing or enhancing immune response or for inhibiting or preventitumor growth.
                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-813972/80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; MHC class I pathway; antigen specific immune response;
E7 protein; E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16
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                61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPBEKQRHLD 120
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                                                                        1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                           99.2%;
                                                                                                            Score 823; DB 8; I
Pred. No. 9.2e-84;
1; Mismatches 2;
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                                                                                                                                          Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                     as a vaccine
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptide is the sequence of the human papillomavirus HPV 16 E6 nucleoprotein. Peptides corresponding to regions (pref. epitopic regions) of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions contg. these peptides, antibodies against the peptides, or recombinant cells contg. the gene encoding the immuno-genic peptides may be utilised in methods for inhibiting and treating HPV infection and tumour initiation and progression e.g. in the prevention or retardation of cervical warts and cervical carcinoma resulting from HPV infection. See also AR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7; 81pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide(8) derived from E6 or E7 region of HPV16 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-132119/16.
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21-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 158 AA;
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                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETOL 151
                                                                                                                                                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                     AVXDXCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                             MFQDPQERPRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PI field.)
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                                                                                                                                                                                                                                                                                           Score 823; DB 2;
Pred. No. 9.7e-84;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment and prophylaxis
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RESULT 10

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                                                                                                                                                                                                                            The present invention describes an agent used in the treatment or prophylaxis of a disease caused or exacerbated by MPV (mammalian parphilomavirus) comprising a compound capable of reducing, inhibiting or otherwise decreasing the activity of a protein encoded by an MPV gene by facilitating disruption of a chelated metal cation domain present in the protein. An agent of the present invention can be used to treat cervical cancer or its HPV associated precursor lesions or other HPV associated cancers and/or warts. The present sequence represents a human papillomavirus E6 protein containing two zinc finger motifs, as given in the exemplification of the present invention
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Polysulfide and dithionodisulfide agents, useful for the treatment prophylaxis of diseases caused by mammalian papillomavirus, are disruptors of a chelated metal cation domain in an MPV gene encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-256917/22
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                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-1998;
15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) INST MOLECULAR & CELL BIOLOGY (HUGH/) HUGHES E J L.
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                                                                                                                                                  Local Similarity
nes 148; Conserv
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                                                                                                                  MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                 AVCDXCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zinc finger; therapeutic; treatment; pr
papillomavirus; antiviral; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tan YJ,
                                                                                                                                                     Conservative
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99AU-00001645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "forms a zinc finger motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "forms a
                                                                                                                                                                                                                                                                                                                                                                      78pp;
                                                                                                                                                                99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E6 protein containing
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                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                    Score 823; DB Pred. No. 9.7e 1; Mismatches
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                                                                                                                                                                823; DB 3;
No. 9.7e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prophylaxis; MPV;
                                                                                                                                                                          Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer; lesion;
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                                                                                                                                                     Indels
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ARESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated prepared human papillomavirus (C (HPV) epicope (I). (I) has antiviral activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the CC present invention are useful for stimulating an immune response to HPV by Stimulating the production of CTL or HTL responses, specifically in the CC treatment or prophylaxis of HPV infection, in persons who have not manifested symptoms e.g. genital warts or neoplastic growth. The peptides CC can also be used in a tetramer staining assay to assess peripheral blood CC mononuclear cells for the presence of antigen-specific CTLs following CC exposure to a pathogen or immunogen, and as reagents to evaluate immune CC compositions are useful for removing warts or treating HPV infections. CC The epitopes for inclusion in an epitope-base vaccine may be selected CC from conserved regions of viral or tumour-associated antigens, which CC reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of CC epitope-base vaccines. An additional advantage is the ability to combine CC epitopes achieving enhanced immunogenicity, the major benefit of the CC vaccine is that is safe and efficacious. AAB9331 to AAB9477 represent CC invention
                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-1999; 99US-0172705P.
15-AUG-2000; 2000US-00641528.
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-381497/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-2000; 2000WO-US033549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus protein HPV16 E6
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                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                  AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                           Score 823; DB 4;
Pred. No. 9.7e-84;
1; Mismatches 2
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Best Local S
                                                                                                                                                                                                                                                                                                                                 Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel purified complex comprising a first polypeptide and a second polypeptide, where the polypeptides comprise defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytostatic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing a conditions involving altered jevel of the complex, e.g. human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases. The sequences shown in ADF09500-ADF09583 represent proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified complex comprising a first polypeptide and a second polypeptide, useful for identifying agents for treating/preventing condition involving altered level of the complex e.g. human papilly virus infection, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 16; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; protein-protein interaction; virucide; cytostatic; vaccine; human papilloma virus; HPV; cancer.
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HOFFMANN LA ROCHE INC.
                                        KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                     AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                                           Score 823; DB 7;
Pred. No. 9.7e-84;
1; Mismatches 2
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RESULT 14
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Matches 148
                                                                                                                                                                                                                                                                                                                                            The invention comprises a nucleic acid molecule (DNA vaccine) that encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MFC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E6 protein of the invention.
AEA40817 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccine for inducing or enhancing immune response or for inhibiting or preventing
                                                                                                                                                                                                                                                                                                                   Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 4; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; MHC class I pathway; antigen
E7 protein; E6 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADU66363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                          148;
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                                                                                                                                                                                                                                                                        Similarity
                                                                                        KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                 AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                     99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
                                                                                                                                                                                                                                                     Score 823; DB 8; I
Pred. No. 9.7e-84;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HPV16)
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Б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                                                                                                                                                                                                                                                    Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                        Indels
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL

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                                                                                                                                                                                                                                                          cc acid vector comprising a first sequence encoding an antigenit polypeptide or peptide, and optionally, a second sequence linked to the first corporation and indicate the first corporation of the sequence and encoding an immunogenicity-potentiating polypeptide (IPP); and a second nucleic acid vector encoding an anti-spoptotic polypeptide. When the second vector is administered with the first vector to a compression of the second vector is administered with the first vector to a competition of the second vector is administered with the first vector to a competition of the first vector alone. The invention further includes a particle comprising an anti-spopential that is suitable for introduction into a cell or an animal by particle composition; a pharmaceutical composition comprising the particle composition; an antigen specific immune response, comprising the particle and a carrier or an excipient; inducing or enhancing an antigen specific immune response of the numbers of CD8+ CTLs composition for a selected desired antigen in a subject; and inhibiting the composition of a tumor in a subject. The nucleic acid composition is useful as an immunogen for inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as an immunogen for inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as compositatic activity. This sequence represents ananti-apoptotic vector HPV composition of the invention.
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                                                                                                                                                Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                            Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid composition comprising a first nucleic acid vector encoding an antigenic polypeptide and a second nucleic acid vector encoding an anti-apoptotic polypeptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2003; 2003US-0449429P.
18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 7; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenicity; immunogenicity-potentiating polypeptide; IPP;
vaccine; immune stimulation; tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENBANK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2004; 2004WO-US005292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-apoptotic vector HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                    Local Similarity
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                                                                                                                                                148;
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                     AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NC_001526.
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                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EG
                                                                                                                                            Score 823; DB Pred. No. 9.7e-
1; Mismatches
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                                                                                                                                                                  823; DB 9;
No. 9.7e-84;
                                                                                                                                                                                  Length 158;
                                                                                                                                                  Indels
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 127
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128 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 158

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RESULT 15
ARA98532
ID ARA98
XX ARA98
XX ARA98
XX PAPI
DT 08-SE
XX PAPI
XX PAPI
XX PAPI
XX PAPI
XX US20(
XX US20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antibody composition comprising a mixture of monoclonal antibodies that specifically bind to 86 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to 86 proteins of at CC diagnostic kit (for detecting an HPV strains. Also included are a diagnostic kit (for detecting an HPV strains. Also included are a comprising the antibody composition above), a method of detecting an HPV CC protein in a sample, a method of detecting the presence of an concegenic HPV 86 protein in a sample and a system for detecting a HPV CC presence of an oncogenic HPV 86 polypeptide in a sample (comprising a first and a second binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the 86 proteins of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 13; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532373P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2005142541-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                       Similarity
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                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                    MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                    MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                         AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                 99.2%;
98.0%;
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                                                                                                                                                                                                                                                                                                                       Score 823; DB 9;
Pred. No. 9.7e-84;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                              Length 158
                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 16
AEB1190
ID AEB11
XX
XX AEB11
XX
XX AEB11
XX
XX AEB11
XX
XX Tunor
KW Tunor
KW Cance
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                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing a synthetic protein of a pathogen or tumor comprises chemically synthesizing two or more fragments of 2-80 contiguous amino acids of sequence, the sequence of two or more fragments are neighboring and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 2; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-497704/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor-associated cancer; HPV16 E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYLE-) UNIV LEIDEN MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                              AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                       MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 9.7e-84;
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                                                                           multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the E1, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchox/spacer paptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chesnut Chen Y,
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02-JUL-2004;
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ds encoding the human papillomavirus (HPV) cytotoxic T
L) epitopes, useful in preparing a vaccine against HPV.
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Deyoung
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HUANG M T F.
POWER S D.
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BABE L M.
CHEN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BABE
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BAKER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWMAN M J.
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2004US-0584652P.
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Juang MTF,
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Power SD;
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RESULT 18
ABC96391
ID ABC96
XX ABC96
XX ABC96
XX ALC96
XX ALC96
XX Human
XX Epito
XX WO200
XX Human
XX GEPIY
PR 03-JA
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Best Local Similarity
construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the
                                                                                                                                                                                                                                                            New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chesnut
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(NEWM/)
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02-JUL-2004; 2004US-0584652P.
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                                                                                                                                                                                                               Disclosure; Page 56; 518pp; English.
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BABE L M.
CHEN Y.
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                                                                                                                                                                                                                                                                                                                                                                                                          Huang MTF,
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Pred. No. 9.7e-84;
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Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Babe
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RESULT 19
AEF88
XX AEF88
XX AEF88
XX AEF88
XX 20-AP
DT 20-AP
XX Vacci
KW Uteri
KW Uteri
KW UUS200
XX 10-AP
PD 23-PE
XX 20-AP
PA (HEAL
XX 20-AP
PA WPI;
XX WPI;
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XX WPI;
XX WPI;
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Matches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a defense is an HPV protein used to derive epitopes for the vaccine of the
The present invention relates to novel fusion protein for inhibiting on preventing cancer induced by human papillomavirus type 16 (HPV16). The fusion protein comprises an E7 peptide sequence of human papillomavirus type 16, a translocating peptide for translocation and a peptide fragme
                                                                                                                            New fusion protein comprising E7 peptide sequence of human papillomavirus type 16, useful for inhibiting or preventing cancer, e.g. cervical or lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; gene therapy; papillomavirus infection; uterine cervix tumor; cytostatic; gynecology and lung tumor; respiratory disease; E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                         Claim 4; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    papillomavirus
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98.0%;
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                                                                                         English
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Pred. No. 9.7e-84;
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peptide fragmen
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     Methods have been developed for distinguishing a subset of human pagilloma virus (HPV) that is associated with an increased risk developing cervical dysplasia or cervical cancer. The methods in (1) preparing a cervical sample to expose any HPV-16 E6 gene in the sample and determining if the base at position 350 of the E6 gene
                                                                                                                                                                                              Evaluating risk of cervical dysplasia or cervical cancer -variant form of human papilloma virus 16. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1994;
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16-FEB-1998
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                                                                                                                                                      Claim 7;
                                                                                                                                                                                                                                                                                                                                               Wheeler
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DB; AAT94723.
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dysplasia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       circular; human papillomavirus type ia; cervical cancer; cervical smear.
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residues are given following on'
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No. 9.7e-84;
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Best Local
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The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine; fusion partner; immunogenicity; HPV infection; neoplasm; HPV16; human papillomavirus-16; EE6T-sequence.
                                                                                                                            (human papillomavirus)
highly immunogenic fusi
                                                                         Disclosure; Fig 2; 34pp; English.
                                                                                                                                                                                                                                                         Cid-Arregui A,
                                                                                                                                                                                                                                                                                                                                  23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 162 AA;
                                                                                                                                                                                                                                                                                                (DEKR-)
                                                                                                                           new DNA sequence encoding a fusion protein comprising a mutagenized HPV human papillomavirus) E6 or E7 coding sequence and a sequence encoding a serial immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                                         2002-724952/79
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Pred. No. 1e-83;
1; Mismatches 2
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RESULT 22
AAR63865
ID AAR63
XX HPV1
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Best Local S
Matches 148
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25-MAR-2003
28-JUN-1995
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   The sequences of the E6 papillomavirus (HPV) 16 proteins in AAR63865-66,
                                                                                                                                                                                                                                                                                                                               WPI; 1995-006821/01.
P-PSDB; AAQ75470.
                                                                                                                                                                                                                        Human papilloma virus detection assay - by amplification using sustained sequence replication and hybridisation with a detecto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR63865;
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                                                                                                                                                    Page 24-26;
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-00058920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=_E6_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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and E7 polypeptide-encoding regions of human and 18 are given in AAQ75470-71 and the enco, respectively. Probes and primers based on the continuation of the continuat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E7_protein
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                                                                                                                                                79pp; English.
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Pred. No. 1.1e-83;
1; Mismatches 2
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RESULT 23
AD044068
ID AD044
XX AD044
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XX IS Amino
XX E6 pr
XW Cervi
XW E6 pr
XW Cervi
XW E7
CO 15-AF
PW W0200
PW 02-OC
XX IS Muman
OS Synth
XX W0200
PW 02-OC
XX IS Muman
OS Synth
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XX IS Muman
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Best Local S
Matches 148
The present sequence represents a fusion protein, comprising E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). The fusion protein is designated E7E6TetM, and comprises an E7 amino terminus (where residues 24 and 26 have been replaced with glycine) and an E6 carboxy terminus (where residues 63 and 106 have been replaced with glycine). B7E6TetM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of
                                                                                                                                                                                                                                                            New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences were used for HPV infection diagnosis; expression of E6 and diagnostic for cervical cancer or pre- malignant states. (Updated c 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardi OS field)
                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                    Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004030636-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anal cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO44068 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-2004
                                                                                                                                                                                                                                                                                                                                                              2004-316328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                           22; Page 73-74; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFQDPQERPRKLPQ1CTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WYETH HOLDINGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLD
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                                                                                                                                                                                                                                                                                                                                                                                                    Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of a fusion protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system cancer; penile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 823; DB 2;
Pred. No. 1.2e-83;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lower gastrointestinal tract cancer; sancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 188
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                                                                                                                                                                                                                                                                                    E7 polypeptides, (HPV) -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on
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                                                                                                                                                      (where
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Best Local Simi
Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                        ων μιστειπ; Ε7 protein; fusion protein; cervical cancer; immune resnonga. learn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                 03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                      02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                                                                                                   WO2004030636-A2
                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a fusion protein designated E7E6PentM
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO44070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO44070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                      2004-316328/29.
DB; ADO44071.
                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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                                                                                                                                                                                                           WYETH HOLDINGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                      Cassetti
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                                                                                                                                                                                                                                                                                                                                                                  cer; immune response; lower
reproductive system cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                                                                                                                                                                  system cancer;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              823; DB 8;
No. 1.7e-83;
                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                        HPV16; HPV-associated cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                  penile cancer; vulvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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polypeptides from human papillomavirus type 16 (HPV16). The fusion protein is designated E7E6PentM, and comprises an E7 amino terminus (where residues 24, 26 and 91 have been replaced with glycine) and carboxy terminus (where residues 63 and 106 have been replaced with glycine). E7E6PentM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and I

replaced with

B7

an

E 6

The present sequence represents a fusion protein,

comprising

87

New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.

E7 polypeptides, (HPV)-associated

Claim

Page 75-76; 101pp;

English

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypoptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypoptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                         Virus-like particle vaccines containing dengue as core for carrier, applicable in preventives like cervical cancer and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; virucide; dengue virus; recombinant replicon; deletion; preM protein; C protein; NS1 protein signal; vaccine; cervical cancer; viral disease; antigen; dendritic cell; immune response;
                                                                                                                                                                  Pang
                                                                                                                                                                                                                                                         30-JAN-2003; 2003CN-00115272.
30-JAN-2003; 2003CN-00115273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR47005 standard; protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the
                                                                                                                                    WPI; 2004-625870/60.
                                                                                                                                                                                                             (SHAN-)
                                                                                                                                                                                                                                                                                                      30-JAN-2004; 2004WO-CN000088
                                                                                                                                                                                                                                                                                                                                    26-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                    WO2004072274-A1
                                                                                                                                                                                              (BEIJ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                                                                                             papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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                                                                                                                                                                                              SHANGHAI TENGEN BIOMEDICAL CO LTD.
TENGEN BIOMEDICAL CO.
BEIJING ORIENTAL TENGEN TECHNOLOGY DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINGQKPLCPEEKQRHLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 16
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 823; DB 8;
Pred. No. 1.7e-83;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for Dengue virus vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                       virus recombinant or/and remedies fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                         for tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
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A dengue virus recombinant replicon has a

deletion of the complete coding

producing a drug for the prophylaxis and treatment of cancer or vi

viral

producing a drug infection.

Example 2;

SEQ ID NO 2; 38pp; Chinese.

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RESULT 26
AEF400157
ID AEF40
XX AEF40
AC AEF40
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 30-JAN-2003; 3
30-JAN-2003; 3
30-JAN-2004; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus can infect dendritic cells, and can effectively present antigen to provide immunity effect. Different types of dengue virus can be used to repeatedly produce efficient immune response thereby strengthening the body's immune system against the pathogen that contains such antigen. Human papillomavirus (HPV) vaccines were prepared by using a gene-expressing system using of the full-length dengue virus cDNA clone (pRS/FLD2). The recombinant virus vectors were transfected into baby hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell lines. This sequence corresponds to the HPV type 16 E7 protein whose encoding gene is used as the gene of interest in the recombinant replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence for preM protein of dengue virus and also includes elements of e.g. the non-coding region in the whole of the 5'-end, the coding region of the front 20 amino acids in the C protein, and the coding region of NS1 protein signal, coding regions of all non-structural proteins. The obtained vaccines are useful in producing preventives or/and remedies for cancer like cervical cancer and viral diseases. Such vaccines can efficiently express antigen in infected cells, which is because dengue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic; neoplasm; viral infection; virucide; infection; oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEF40157 standard; protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding gene is of the invention.
                                                                                                                      N-PSDB; AEF40156.
                                                                                                                                                   WPI; 2006-109169/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2006018928-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2005; 2005US-00192923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-2006.
                                                                                                                                                                                                                                                                             (PANG/)
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                                                                                                                                                                                                                                                                                                                                    2003CN-00115272.
2003CN-00115273.
2004WO-00072274.
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98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 16.
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Best Local
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25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a virus-like particle (VLP) vaccine which contains dengue virus (DEN) recombinant replicon as its core. The DEN replicon contains exogenous nucleotide sequences such as human papillomavirus (HPV) antigen proteins, immune regulators or combination of HPV antigen and immune regulators. The invention is useful for producing a drug for the prophylaxis and treatment of cancer or viral infection. The present sequence is a human papillomavirus oncoprotein.
                                             Recombinant virus vectors encoding human papillomavirus proteins - for treating and vaccinating against HPV infections and conditions caused them, such as cervical cancer.
                                                                                            WPI; 1992-349219/42.
N-PSDB; AAQ29389.
                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                          Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR27725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR27725 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 256 AA;
                                                                                                                               Boursnell MEG,
                                                                                                                                                                                                     10-MAR-1992;
                                                                                                                                                                                                                                                   WO9216636-A1
                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                    HPV 16
                                                                                                                                                      (IMMU ) IMMUNOLOGY LTD
                                                                                                                                                                              14-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                               immunotherapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                   E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFQDFQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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(revised)
(first en
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                                                                                                                               Inglis
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1. .159
                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; 24pp; English
                                                                                                                                                                                                                                                                        "HPV-16 E6 protein"
                                                                                                                               SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263
                                                                                                                                Munro
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Pred. No. 1.7e-83
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The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd.

Disclosure; Fig la; 83pp; English.

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RESULT 28
AAR97561
ID AAR97
XX AAR97
XX AAR97
XX 27-AU
DT 27-AU
DT 11-JA
XX Human
XX
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Best Local Similarity 98.0
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using oligonuclectides SO5 and SO6. The prod. of the third reading frame is the HPV-16 E6 protein whereas the second reading frame encodes HPV-16 E7. The E6 and E7 ORFs are fused together to form a single continuous ORF via site directed mutagenesis and the immortilising potential of E7 is removed by altering two key codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites (pref. by inserting two sets of the DNA in opposite orientations to overcome the problem of intertypic recombination) to make a recombinant virus vector for use immunotherspeutically to activate cells of the immune system against HPV. See also ARR27723-43. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                       WPI; 199
A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be in vaccines against HPV or to treat HPV infection. The variant is
                                                                                                                                                                              Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection.
                                                                                                               Example 1; Page 15-16; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Edwards SJ, Cox J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papilloma virus; E6; E7; deletion mutant; HPV; immune humoral immune response; cellular immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papilloma virus E6/E7 protein variant
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11-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                   1996-309518/31.
DB; AAT31833.
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(first entry)
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Pred. No. 1.8e-83;
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Best Local Similarity
                           AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAX28375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonuclectide. The products of the invention can be used to induce ar immune response in a patient to an HPV antigen. They can also be used f preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preferably a deletion mutant comprising at least half, and preferably two rethirds of full length E6 or E7 protein starring from the N- or C- terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a full length E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                 Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                  Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                       WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY25376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen;
                                                                                                                                                                                                                       1999-405485/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148;
                                                                                                                                                                                                                                                                                                                                                                                                               papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                             SMITHKLINE
                                                                                                                                      II; Page 48-49; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFODPOERPRKLPOLCTELOTTIHDIILECVYCKOOLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein D1/3-E6-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                  Gerard
                                                                                                                                                                                                                                                                                                       97GB-00027262
                                                                                                                                                                                                                                                                                                                                  98WO-EP008563
                                                                                                                                                                                                                                                                             BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        partner; CpG of
ion; treatment
                                                                                                                                                                                                                                                  CMG
                                                                                                                                                                  to
to
                                                                                                                                                                  HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 823; DE
Pred. No. 1.8e
1; Mismatches
                                                                                                                                                                                E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CpG oligonucleotide; immune response;
                                                                                                                                                                                or E6/E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 823; DB 2; Le
. No. 1.8e-83;
ismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 158
                                                                                                                                                                                fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Sequence

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MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY

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         Query Match
Best Local
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Best Local
                                                              This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus. Haemophilus influenza
                                                                                                                                                                 Disclosure; Fig 3; 95pp; English.
                                                                                                                                                                                        treatment
                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                            22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                            WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric, E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prot.D1/3-E6-His/HPV16 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY02632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02632 standard;
                                                                                                                                                                                                                                                       Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                      SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                  1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                     Papilloma Virus (HPV)
ment or prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
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                                                                                                                                                                                                                       AAX29781.
                                                                                                                                                                                                                                                                                                                                                                                                                                           lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKQREHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                           273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDI
                                                                                                                                                                                                                                                                                                                                                                                                             influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E7; fusion protein;
                                                                                                                                                                                                                                                                                                             97GB-00017953
                                                                                                                                                                                                                                                                                                                                  98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                                                                                                           benign;
                                                                                                                                                                                                                                                                 Silva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
          99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                 'n
                                                                                                                                                                                                                                                                                                                                                                                                                                           malignant;
                                                                                                                                                                                      HPV induced lesions
                                                                                                                                                                                                                                                                 Delisse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273
Score 823; DB 2;
Pred. No. 1.9e-83;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 823; DB 2;
Pred. No. 1.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                            protein D; vaccine
; virus; infection
                                                                                                                                                                                                                                                                 AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                 Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                useful
                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                 in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
                       273;
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RESULT 31
ARD52634
ID ARD522
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                                                                                                                                                                                                          Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-557648/57.
N-PSDB; AED52633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein D1/3-E6-His/HPV16.
                                                                                                                                                                                                                                                                                                                   Sequence 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 3; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN9801903-I4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae; strain 772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AED52634 standard; protein; 273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                         114
                                                                                                                                                                                                            148;
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                                                 61
                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                     99.2%;
                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                          Pred. No. 1.9e
1; Mismatches
                                                                                                                                                                                                                                   Score 823; DB 9;
Pred. No. 1.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; papillomavirus infection; D protein.
                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            <u>,,</u>
                                                                                                                                                                                                          Gaps
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Matches 148
                                                                                                                                                                                                                                                 AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response; HPV antigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV fusion protein CLYTA-E6-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY25379;
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                     Example VI; Page 52-53; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising an E6, induce immune response to HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                     193
                         121
                                                                                                            133
                                                                                61
                                                                                                                                                                    148;
                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX78795
                                                                                                          MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 192
                                                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                      AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                     AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                           292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                              99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ල</u>
බ
                                                                                                                                                                 Score 823; DB 2;
Pred. No. 2e-83;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                              E7 or E6/E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
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                                                                                                                                                                                                                                                                                                                                                                                                                fusion
                                                                                                                                                                   2
                                                                                                                                                                                             Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 from HPV to
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RESULT 33
AAY02635
ID AAY02635 standard; protein; 292

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RESULT 34
AED52642
ID AED52
XX
AC AED52
XX
AC AED52
XX
DT 29-DE
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus gneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric; E6; E7; fusion processing the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Papilloma Virus (HPV) fusion proteins - useful in vaccines treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruck C, Cabezon S
Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus. Streptococcus pneumoniae.
                      Fusion protein
                                                                         29-DEC-2005
                                                                                                                         AEDS2642;
                                                                                                                                                                       AED52642 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 10; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY02635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLYTA-E6-His protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                               KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                             AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AA;
                                                                                                                                                                                                                                                                                              KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first en
                                                                       (first entry)
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                           cLytA-E6-His/HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۶
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t; virus;
                                                                                                                                                                          292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 823; DB 2
Pred. No. 2e-83;
1; Mismatches
                                                                                                                                                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLYTA; vaccine; immunotherapy; tumour; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 292;
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RESULT 35
AAY25377
ID AAY25
XX AAY25
AC AAY25
XX O6-SE
XX PO6-SE
XX FUSIO
KW FUSIO
KW FUSIO
KW HPV a
XX Synth
OS Synth
XX HUMan
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Best Local Similarity
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                   HPV fusion protein D1/3-E6E7-His/HPV16
                                                                                                                                                                                AAY25377
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E7;
                                                                           Fusion
                                                                                                                              06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Fig 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
                                                               usion protein; E6 protein; E7 protein; immunological fusion partner; CpG oligon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK)
                                                 antigen;
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DB; AED52641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                  MFQDPQERPRKLPQLCTELQTT1HDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                               standard; protein;
                                                                                                                                                                                                                                                 KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                  AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                 prevention; treatment.
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-00179535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type
                                                              rotein; E7 protein; E6/E7; immunomodulator; tumour;
partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                  371
                                                                                                                                                                                                                                                                                                                                                                                                      Score 823; DB 9
Pred. No. 2e-83;
1; Mismatches
                                                                                                                                                                                  $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; papillomavirus infection; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                 283
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                292
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                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                    252
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Synthetic

Human papillomavirus

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RESULT 36
AAY02633
ID AAY02
XX AAY02
XX AAY02
XY 17-OC
DT 17-OC
DT 22-JU
XX Chime
KW Cunnou
XX Chime
KW tunnou
XX Humar
OS Haemm
COS Chime
XX WO991
XX PP 17-AI
XX XX
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Best Local Sim
Matches 148;
                                                                                                                      Human papillomavirus. Haemophilus influenzae. Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for
                                                                                                                                                                        Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy; tumour; lesion; benign; malignant; virus; infection.
                                                                                                                                                                                                                                            17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dalemans WLJ, Gerard CMG;
                                        17-AUG-1998;
                                                                                                                                                                                                                 Prot.D1/3-E6-E7-His/HPV16 protein
                                                                                                                                                                                                                                                                                     AAY02633;
                                                                                                                                                                                                                                                                                                             AAY02633 standard; protein; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example III; Page 50; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1998;
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               22-AUG-1997;
                                                                                            WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-405485/34.
DB; AAX78793.
                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97GB-00027262
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               97GB-00017953
                                        98WO-EP005285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 823; DB 2;
Pred. No. 2.7e-83;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or E6/E7 fusion protein from HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                          RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruck C, Cabezon S
Lombardo-Bencheikh
 WPI; 2005-557648/57.
N-PSDB; AED52637.
                                                                                  22-AUG-1997;
                                                                                                         24-AUG-1998;
                                                                                                                                                                                           Human papillomavirus Synthetic.
                                                                                                                                                                                                                                        Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E7;
                                                                                                                                                                                                                                                                           Fusion protein D1/3-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                    29-DEC-2005
                                                                                                                                                                                                                                                                                                                            AED52638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                    Tyrrell AWR
                                                                                                                                 04-MAR-2005
                                                                                                                                                       IN9801903-I4
                                                                                                                                                                                                                  Haemophilus
                                                                                                                                                                                                                                                                                                                                                  AED52638 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                          (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                          SMITHKLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                              KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                               KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                  influenzae; strain
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                  97EP-00179535
                                                                                                          98IN-CH001903
                                                            BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.2%;
                                                                                                                                                                                                       type
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                                                                                                                                                                                                                                                                                                                                                    371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 823; DB 2;
Pred. No. 2.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                    $
                                                                                                                                                                                                                                         cytostatic; papillomavirus infection; D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                264
                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 371;
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RESULT 38
AAY25381
ID AAY25
AC AAX78
AC AAX78
AC AAX78
AC AAX78
AC AAX78
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (20-127) the C-terminus of the equence represents an HPV-H. influenzae D protein, fusion protein of the
                                                  Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY25381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine
  AAX78791-X78801
                           Example VIII; Page 55-56;
                                                                                                                              Dalemans WLJ,
                                                                                                                                                                                                          18-DEC-1998;
                                                                                                                                                                                                                                                               WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                       Fusion
                                                                                                                                                                                                                                                                                                                                                                              HPV fusion protein CLYTA-E6E7-His/HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY25381 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                     08-JUL-1999.
                                                                                                                                                                                                                                                                                                                             antigen;
                                                                                         1999-405485/34.
DB; AAX78797.
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                                                                                                                                                                                                                                                                                       papillomavirus
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                                                                                                                                                                                                                                                                                                                                          l protein;
logical fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zion relates to human Papilloma virus (HPV) fusion proteins, an immunological fusion partner that provides T helper epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                             prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                           fusion
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                                                                                                                               Gerard
                                                                                                                                                                                 97GB-00027262.
                                                                                                                                                                                                           98WO-EP008563
                                                                                                                                                                                                                                                                                                                                        E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
usion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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98.0%;
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                         62pp;
                                                    E6,
  nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 823; DB 9; Pred. No. 2.7e-83;
                                                                 E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                           English
                                                               or E6/E7
acid sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264
                                                                 fusion
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                                                               protein
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Best Local Similarity
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      protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours
                                                                                                                                          Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                      Bruck C, Cabezon S
Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus Streptococcus pneumor
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric; E6; E7 lesion; benign;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                 Disclosure; Fig 14;
                                                                                                                                                                                               WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                               17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                         04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLYTA-E6E7-His protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY02637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY02637
                                                                                                                                                                                                                                                                                       22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                WO9910375-A2
                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                   AAX29786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                   Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7;
                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                        97GB-00017953
                                                                                                                                                                                                                                                                                                                 98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                                                                                                              malignant;
                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion protein;
alignant; virus;
                                                                                                                95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%;
                                                                                                                                                                                                                                   Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 823; DB
Pred. No. 2.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLYTA; vaccine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
.9e-83;
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                                                                                                                                                                                                                                   Gerard CMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunotherapy;
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                                                                                                                                                         in vaccines
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RESULT 40
AED52646
ID AED52
XX AED52
XX AED52
XX Pusio
XX Pusio
XX Pusio
XX Pusio
XX Pusio
XX Pusio
XX Chime
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OS Synth
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XX IN98C
XX INFI;
DR WPI;

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                                                       Matches 148;
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 148;
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Best Local Similarity
                                                                                                                                                                                                               The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epicopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lych protein (cLych) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-557648/57.
N-PSDB; AED52645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pusion protein; vaccine; virucide; uterine cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AED52646 standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Fig 14; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein cLytA-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AED52646
                                                                                                                                                                Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN9801903-I4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accine; papilloma; cytostatic; papillomavirus infection; cervix tumor; E7; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.2%;
                                                                              99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 823; DB 2;
Pred. No. 2.9e-83;
1; Mismatches 2
                                                    1; Mismatches
                                                                              Score 823; DB 9;
Pred. No. 2.9e-83;
                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 390
                                                                                                         Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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FQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYA

Query Match Best Local (Matches

Similarity

98.9%;

Score 821; DB Pred. No. 2.8e 0; Mismatches

e 821; DB 8; Le . No. 2.8e-83; ismatches 2;

Length 248; Indels

0

Gaps

61 0

148;

Conservative

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RESULT 41
AD044066
ID 410044
XX AD044
XX AD044
XX AMINO
XX B6 pr
KW Eervi
KW anal1
XX Human
OS Synth
XX W0200
PD 15-AF
XX 02-OC
XX 03-OC
XX WPI
DR N-PSI
XX WPI
DR WFT
CANCIO
CC The |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     중*: 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                             The present sequence represents an E7B6 fusion protein, comprising wild CC type E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). CC The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any CC one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are CC useful for treating or preventing human papillomavirus (HPV)-associated CC cancers, such as cervical cancer. The fusion proteins and nucleic acids CC encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 16. Synthetic.
Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 72-73; 101pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADO44067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-316328/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of an E7E6 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
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AAY57808
ID AAY57
XX AAY57
XX AAY57
XX 20-MA
XX Trans
KW Creb
KW Creb
XX Vival
XX Uvival
XX Humar
XX Humar
XX 26-MA
YX 2
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                                                                                                                                                                                                  The present invention describes a polypeptide comprising a Ctranscriptional adaptor motif (TRAM) or a TRAM-interaction motif (TRIM) CC (I). (I) can be used for identifying compounds (II) comprising a CC (I). (I) can be used for identifying compounds (II) comprising a CC polypeptide capable of disrupting an interaction between a TRAM sequence and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a CC TRIM sequence are identified by incubating, the polypeptide with (I) and CC determining if the polypeptide interacts with (I). Compound (II) is CC useful for preparing a pharmaceutical composition and for disrupting an interaction between TRAM sequence and TRIM sequence in vitro, thereby CC inhibiting viral transcription or cell cycle progression in mammalian CC cells especially cancer cell. Compounds which disrupt interaction between CC TRIM/TRAM containing polypeptides can be used therapeutically to prevent CC or treat viral diseases and tumours. The polypeptides reduce conceptibility of cells to viral infection and regulate cell cycle concluding apoptosis and growth arrest and can be used to produce concluding apoptosis and growth arrest and can be used to produce continuous against the TRIM or TRAM sequences. HPV types associated with risk or low risk of cervical cancer can be distinguished based on the ability of E8 polypeptides to bind to creb binding protein (CBP) TRAM sequence. The present sequence represents a HPV-16 E6 protein amino acid conception and regulate cell cycle can be used to produce the ability of E8 polypeptides to bind to creb binding protein amino acid conception and regulate cell cycle can be used to produce the ability of E8 polypeptides to bind to creb binding protein amino acid cycle sequence from an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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   Query Match
Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               creb binding protein; transcriptional regulation; cytostatic; antiviral; cell cycle inhibitor; viral transcription inhibitor; cancer; tumour; viral disease; viral infection; cell cycle; apoptosis; growth arrest.
                                                                                                                                                 Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides cells useful for treating viral disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'connor MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1998;
05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcriptional adapter motif; TRAM; TRAM interaction motif;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV-16 E6 protein amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY57808,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-072620/06
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                                 98.6%;
Score 818; DB 3; Length 151; Pred. No. 3.3e-83; 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                 Matches 147;
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response to an antigen in a patient. The method comprises administe to the patient an immunoglobulin (Ig) or its portion where the Ig is least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1G; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2002; 2002US-0412219P.
14-MAR-2003; 2003WO-US007995.
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                                                                                                                          AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                   MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                           KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                AVCDKCLKFYSKISEYRYYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                                                                                                          MFQDPQERPRKLPHLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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Conservative
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                                                                                                                                                                                                                                          The invention relates to an antitumour composition containing a therapeutic or prophylactic agent or one or more immunogenic polypeptides, where at least one polypeptide is modified so that its intracellular localisation is different from that of the native polypeptide. This sequence represents an example of a modified immunogenic protein and corresponds to the E6 protein from human papillomavirus fused to the measles virus protein F signal peptide. The compositions, vectors and particles are used to treat or prevent cancers and tumours, specifically those associated with papillomavirus infection (e.g. cancer or low grade dysplasia of the cervix uteri). (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antitumour composition containing immunogenic polypeptide with altered localisation - or vector expressing this polypeptide, particularly for treating or preventing cervical cancer associated with human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antitumour; immunogen; intracellular localisation; cancer; dysplasia; signal peptide; papillomavirus; infection; cervix uteri.
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                                                                                                                                                                                                                   Sequence 243
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16;
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21-MAY-1999
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 181
              KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                      AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPL-----QRHLD
                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                              Page 54-55; 74pp; French.
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nilarity 94.7%;
Conservative
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                                                                                                                                                            Score 779.5; DB 2;
Pred. No. 1.2e-78;
1; Mismatches 2;
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                                       E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR40919
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus; HPV; benign; malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV E6 region product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR40919 standard;
                                                                                                                                                                                                                    Amino acid
                                                                                                                                                                                                                                                                                                  15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                     ADO44077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO44077 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probes are designed to virus. The probes bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 16-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting benign and/or malignant human papilloma virus - by detecting DNA sequence of E6 and/or E7 region of human papilloma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ48575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EKKRFHNIGGRWTGRCMSCWKP--TRRETEV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 71.5
108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GVCMKCLKFYSKISEYRRYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGQPY
                                                                                                                                                                                                                sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.9%; Score 580; DB 2;
71.5%; Pred. No. 1.5e-56;
Itive 13; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detect benign and/or malignant human papilloma to the E6 and/or E7 region of human papilloma
                                                                                                                                                                                                                E6 polypeptide of HPV35
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AEA98533
ID AEA98
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XX Papil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for representing immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
 US2005142541-A1
                                 Human papillomavirus;
                                                                                Papillomavirus
                                                                                                                                                     08-SEP-2005
                                                                                                                                                                                                                   AEA98533 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003; 2003WO-US031726
                                                                                                                   HPV (oncogenic
                                                                                                                                                                                     AEA98533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 80; 101pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-316328/29.
DB; ADO44104.
                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 69.6%; al Similarity 71.5%; 108; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                    cervix
                                                                                                                                                                                                                                                                                                      EKKRFHNIGGRWTGRCMSCWKP--TRRETEV 149
                                                                                                                                                                                                                                                                                                                        KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                     GVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE
                                                                                                                                                                                                                                                                                                                                                                                          AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFQDPQERPRKLPQLCTELQTT1HDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĀΑ;
                                                                                                                                                    (first entry)
                                                                  tumor; cytostatic.
                                                                                infection; virucide;
                                                                                                                   strain) E6 amino acid sequence SEQ ID 14.
                                 etrain 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 578; DB 8; I; Pred. No. 2.5e-56; 13; Mismatches 28;
                                                                                   9
E
                                                                                 protein; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E7 polypeptides, (HPV)-associated
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RESULT 48
ADF31985
ID ADF31
XX
AC ADF31
XX
T2-FE
DT 12-FE
DT Humar
XX
DE Humar
XX
Homo
OS Homo
XX
CN13E
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PD 27-NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC clast three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV betains a method of detecting an HPV CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC oncogenic HPV E6 polypeptide in a sample (comprising a CC irst and a second binding partner for an oncogenic HPV E6 polypeptide. CC where the first binding partner is a PDZ domain protein and the second CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                              Human papillomavirus fusion gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                        Homo sapiens
                                                                                                                          human papillomavirus; cervix cancer
                                                                                                                                                                                                   12-FEB-2004
                                                                                                                                                                                                                                       ADF31985;
                                                                                                                                                                                                                                                                         ADF31985 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 14; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                  EKKRFHNIGGRWTGRCMSCWKP--TRRETEV
                                                                                                                                                                                                                                                                                                                                                                                                                                     GVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.6%;
71.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;; Score 578; DB
;; Pred. No. 2.5e
13; Mismatches
                                                                                                                                                                                                                                                                           180 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; L
2.5e-56;
1es 28;
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60 60

27-NOV-2002

CN1381583-A.

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ARBSULT 49
ARB98434
ID ARB98
XX ARB98
XX 22-AU
XX Human
XX Human
XX Human
XX Human
XX Human
XX Human
XX 10-DE
PR 11-DE
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PR 15-AU
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human papillomavirus E6/E7 fusion gene, its preparing process, the process for configuring the efficient expression carrier containing the gene and resultant expression carrier, the fusion protein prepared from the gene, and the application of the fusion gene and expression protein to medical science and medicine to treat cervix cancer are disclosed. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus E6/E7 carrier and fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-258260/26.
N-PSDB; ADF31984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus protein HPV31 E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 2; 16pp; Chinese.
                      An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
                                                                                                                                                           Sette A,
                                                                                                                                                                                                                                                                                                                                                  11-DEC-2000; 2000WO-US033549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200141799-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98434 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human papillomavirus fusion gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2002; 2002CN-00117143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2002; 2002CN-00117143
                                                                                                        WPI; 2001-381497/40.
                                                                                                                                                                                                                                                                   10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001.
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                                                                                                                                                                                                                   (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVCDKCLKFYSKISEYRHYRYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MFQAPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVGAFAFRDLCIVYRDGNPY
                                                                                                                                                           Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.9%;
                                                                                                                                                             Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 572; DB 7;
Pred. No. 1.5e-55;
1; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                             Chesnut
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                                                                                                                                                             Celis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 180;
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                                                                                                                                                             Grey
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ARESULT 50
AD044075
ID AD044075
AC AD044
XX AD044
XX AD15-JU
XX B6 px
KW Cervi
KW anall
XX M0200
XX W0200
XX O2-OC
XX O3-OC
XX X W01;
BR (AMHE
XX WD1;
BR WD1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the present invention are useful for stimulating an immune response to HPV by stimulating the production of CTL or HTL responses, specifically in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The epitopes for inclusion in an epitope-base vaccine may be selected from conserved regions of viral or tumour-associated antigens, which reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-base vaccines. An additional advantage is the ability to combine selected epitopes (CTI and HTIL) and to modify the composition of the epitopes achieving enhanced immunogenicity, the major benefit of the vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent polypeptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment or prophylaxis of HPV infection, in persons who have not manifested symptoms e.g. genital warts or neoplastic growth. The peptide can also be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen, and as reagents to evaluate immune recall responses or evaluate the efficacy of a vaccine. The vaccine compositions are useful for removing warts or treating HPV infections.
                                                                                                                                                                                                                                                                                                             cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide invention
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                                                                                                                                                                                                                                                                        Human papillomavirus type 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO44075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO44075 standard; protein; 149
  WPI; 2004-316328/29
                                    Smith L,
                                                                                                                  03-OCT-2002; 2002US-0415929P
                                                                                                                                                         02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                15-APR-2004.
                                                                                                                                                                                                                                     WO2004030636-A2
                                                                                                                                                                                                                                                                                                                                                      E6 protein;
                                                                                                                                                                                                                                                                                                                                                                                               Amino acid
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                                                                              (AMHP ) WYETH HOLDINGS CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVCTKCLRFYSKVSEFRWYRYSVYGTTLEKLTNKGICDLLIRCITCQRPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKKRFHNIGGRWTGRCIACWR--RPRTETQV
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                                       Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                    E7 protein; fusion protein; HPV; HPV-associated cancer;
                                                                                                                                                                                                                                                                                                                                                                                           sequence of the E6 polypeptide of HPV31.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 523; DB 4; ]
Pred. No. 3.6e-50;
B; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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AEA98277 51
AEA98237
ID AEA98
XX AEA98
AC AEA98
AC AEA98
XX Papil
KW Papil
KW Cance
XX US200

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   New antibody composition for oncogenic strains of
                                                                                                                                                                                                                                                                     23-DEC-2003;
                                                                                                                                                                                                                                                                                                                            23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005142541-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus cancer; cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPV (oncogenic strain) E6 amino acid sequence SEQ ID 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEA98537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADO44102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide comprising human papillomavirus E6 and E7 polypeptides, ful for treating or preventing human papillomavirus (HPV)-associated
                                                                                            2005-457781/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WEODPOERPRKT-POLCTELOTTIHDIILECVYCKOOLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                including penile and vulvar cancer.
                                                                                                                                                                                                             ARBOR VITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                Garman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVCTKCLRFYSKVSEFRWYRYSVYGTTLEKLTNKGICDLLIRCITCQRPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKKRFHNIGGRWTGRCIACWR--RPRTETQV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFKNPAERPRKLHELSSALEIPYDELRLNCVYCKGQLTETEVLDFAFTDLTIVYRDDTPH
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                                                                                                                                                                                                                                                                     2003US-0532373P
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                                                                                                                                             JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; virucide; E6 tumor; cytostatic.
                                                                                                                                                   Belmares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
comprising a mixture of monoclonal human papilloma virus, useful for o
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Pred. No. 3.6e-50;
8; Mismatches 33
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                                                                                                                                                   Somoza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; diagnosis; antibody;
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                                                                                                                                                   Schweizer
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   diagnosing
                                 antibodies
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RESULT 52
AEC98865
ID AEC98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC cleast three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC concogenic HPV E6 protein in a sample and a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second CC where the first binding partner is a PDZ domain protein and the E6 proteins CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 98
                                                             (INNO-)
(CHES/)
(NEWM/)
(MOTH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 149
                                                                                                                                                                                                                03-JAN-2005;
                                                                                                                                                                                                                                                                                                                                          Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 18; 161pp; English.
 (BAKE/)
(SOUT/)
(BABE/)
(CHEN/)
                                                                                                                                                               02-JUL-2004;
                                                                                                                                                                              31-DEC-2003;
                                                                                                                                                                                                                                                                               WO2005089164-A2
                                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                         HPV_31 Envelope protein E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEC98865 standard; protein; 149
                                                                                                                                (EPIM-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
98; Conser
SOUTHWOOD
BABE L M.
CHEN Y.
                                                 MOTHE B.
BAKER D.
                                                                                              INNOGENETICS NV. CHESNUT R.
                                                                                                                                EPIMMUNE INC
                                                                               NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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2004US-0584652P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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64.9%; Pred. No. 3.6e-50;
Live 18; Mismatches 33
                                                                                                                                                                                                                                                                                                             type 31.
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RESULT 53
AEC96405
ID AEC96
XX AEC96
XX AEC96
XX D1-DE
XX D1-DE
XX HPV p
XX Human
KW Human
KW epitc
XX epitc
XX PU WO200
XX PD 29-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (C (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that C are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the c multi-epitope construct, a polypeptide comprising an amino acid sequence cc encoded by the polynucleotide, a composition (comprising the comprising the polynucleotide, vector or polypeptide and a carrier), a cell comprising the polynucleotide, vector or polypeptide, inducing an composition (comprising the polynucleotide, vector or polypeptide), inducing an composition composition (comprising the polynucleotide, vector or polypeptide. The epitopes are derived from the composition for the context of the composition that the vector or polypeptide. The epitopes are derived from the composition that tables referred to composition the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune composition to the chales referred to response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition in a composition for inducing an immune composition in the chales providing and thus providing the topic provides the composition to the c
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Matches
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Best Local
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                                                                                                                             Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
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(HUAN/)
(POWE/)
                                                                                                                                                                                               HPV protein
                                                                                                                                                                                                                                             01-DEC-2005
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                                                                                                                                                                                                                                                                                                                             AEC96405 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 149
    29-SEP-2005
                                             WO2005089164-A2
                                                                                    Human papillomavirus
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Deyoung LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                 E6 from HPV31.
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                                                                                                                                                                                                                                             entry)
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64.9%; Pred. No. 3.6e-50;
Live 18; Mismatches 33
                                                                                    type 31
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Juang MTF,
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Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 149;
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RESULT 54 AAB98447 ID AAB98

AAB98447 standard; protein; 149

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                                                                                                                                                                                                                                                                     CC construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes eg., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the cC polynucleotide, vector and/or polypeptide and a carrier), a cell CC polynucleotide, vector or polypeptide, inducing an CC immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide), inducing an CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The cPitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to CC in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune CC response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition in the present provide is an HPV protein used to derive epitopes for the vaccine of the composition in the present composition is an HPV protein used to derive epitopes for the vaccine of the composition.
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                                                                                                                                                                                                                                                                   Sequence 149
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02-JUL-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a new polynucleotide comprising a multi-epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BAKE/)
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BAKER D.
SOUTHWOOD S.
                                                                                                                                                                                                                  Similarity
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CHEN Y.
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                   KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                  AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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KKKRFHNIGGRWTGRCIACWR--RPRTETQV
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64.9%; Pred. No. 3.6e-50;
tive 18; Mismatches 33
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Power SD;
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Best Local (
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the present invention are useful for stimulating an immune response to HPV stimulating the production of CTL or HTL responses, specifically in the treatment or prophylaxis of HPV infection, in persons who have not manifested symptoms e.g. genital warts or neoplastic growth. The peptides can also be used in a tetramer staining assay to assess peripheral blood mononnuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen, and as reagents to evaluate immune recall responses or evaluate the efficacy of a vaccine. The vaccine compositions are useful for removing warts or treating HPV infections. The epitopes for inclusion in an epitope-base vaccine may be selected.
                                                                                                                                                                                                                                                                                                                                               from conserved regions of viral or tumour-associated antigens, which reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-base vaccines. An additional advantage is the ability to combine selected epitopes (CTL and HTL) and to modify the composition of the epitopes achieving enhanced immunogenicity, the major benefit of the vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent polypeptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart;
                                                                                                                                                                                                                                                                                               Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 756pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2000; 2000WO-US033549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200141799-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus protein HPV33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98447;
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121
                                 121
                                                                    61
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                                                                                                                                                                                                                                        Similarity
                                                                  GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                              MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
LNKRFHNISGRWAGRCAACWRS--RRRETAL 149
                           KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                          MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
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                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                    62.7%; Score 520; DB 4; Length 149; 63.6%; Pred. No. 7.9e-50; tive 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
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RESULT 55
ADO44076
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                                                                                                                                                                                                                                                                                                       CC AD044074-AD044085 represent E6 polypeptides from human papillomaviruses. CC AD044098 is the consensus sequence derived from these polypeptides. The gpecification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in CC AD044073 and the E6 polypeptide has no mutations or has mutations at any CC one or more of the amino acids corresponding to amino acids 63 or 106 of CC there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated CC cancers, such as cervical cancer. The fusion proteins and nucleic acids CC encoding the fusion proteins are useful for generating immune responses CC against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive SC system, including penile and vulvar cancers.
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO44076 standard; protein; 149
                                                                                                                                                                                                                                                                           Sequence 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
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121
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                                                                                                   13
                                                                                     MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
                                KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                 GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                        MEQDEQERERKLEQUETELQTTIHDIILECVYCKQQLLRREVYDEAFRDLCIVYRDGNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of the E6 polypeptide of HPV33
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                           62.7%;
                                                                                                                                                                                                          19;
                                                                                                                                                                                                          Score 520; DB 8;
Pred. No. 7.9e-50;
9; Mismatches 34
                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                         Length 149;
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RESULT 56
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 16; 161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody composition comprising a mixture of monoclonal for oncogenic strains of human papilloma virus, useful for o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ARBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-2003; 2003US-0532373P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papillomavirus infection; virucide; E6 protein; diagnosis; antibody; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPV (oncogenic strain) E6 amino acid sequence SEQ ID 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2005
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121
                                                       121 KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARBOR VITA CORP.
                                                                                                                                                               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                   MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                        GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                                                                                                MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  62.7%;
                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                 Score 520; DB 9;
Pred. No. 7.9e-50;
9; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
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                                                                                                                                                                                                                                                                                                                                                                     34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 149;
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diagnosing
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RESULT 57 AEC96412

Matches

Conservative

19;

Mismatches

62.7%; Score 520; DB 9; 63.6%; Pred. No. 7.9e-50;

Length 149; Indels

2

Gaps

1,

Best Local Similarity

Query Match

Sequence

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The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the CC (comprising the polynucleotide, a composition (comprising the CC (comprising the polynucleotide, vector or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an CC immune response against human papillomavirus virus (HPV) and making the CC different strains of HPV and are from the El E2, E6 and E7 proteins. The CC different strains of HPV and are from the El E2, E6 and E7 proteins. The CC citypeptide is useful in preparing a composition for inducing an immune CC compose against human papillomavirus virus (HPV) and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a composition and thus providing a composition in the vaccine of the present composition in the vaccine of the present composition in the vaccine of the composition and thus providing a composition in the present composition in the vaccine of the composition in the vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
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02-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 61; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chesnut
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BAKER D.
SOUTHWOOD S.
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CHEN Y.
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INNOGENETICS NV.
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149
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2004US-0584652P.
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Power SD;
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RESULT 58
AEC98866
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construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.El.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The
                                                                                                                                                                                      New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-2003;
02-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 33
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                                                                                                                                       The invention relates to a new polynucleotide comprising a multi-epitope
                                                                                                                                                                                                                                          WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                      (BAKE/)
(SOUT/)
(BABE/)
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                                                                                                                                                                                                                                                                                                       (DEYO/)
(HUAN/)
(POWE/)
                                                                                                                                                                                                                                                                                                                                            CHEN/)
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DEYOUNG L M.
HUANG M T F.
POWER S D.
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                                                                                                                                                                                                                                                                                                                                                                                BAKER
                                                                                                                                                                                                                                                                                                                                                                     SOUTHWOOD S
                                                                                                                                                                                                                                                                                                                                                                                                       NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                      CHESNUT R
                                                                                                                                                                                                                                                                                                                                                                                                                                INNOGENETICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNKRFHNISGRWAGRCAACWRS--RRRETAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                   monoclonal antibodies that specifically bind to E6 proteins of human papilloma virus (RPV) strains 16, 18, 31, 33 and 45, where at least of the monoclonal antibodies specifically binds to E6 proteins of at least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV E6 polypeptide in a sample, comprising the antibody composition above), a method of detecting an E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the sequence.
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                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 360; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                              New antibody composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV (oncogenic strain) E6
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                                                                                                                                                                                                                                          The invention relates to an antibody composition comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garman JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNKRFHNISGRWAGRCAACWRS--RRRETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain 67
                                                                                                                                                                                                                                                                                                                                                                              comprising a mixture human papilloma virus
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No. 7.9e-50;
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                                                                                                                                                                                                                                                                                                                                                                                diagnosing
                                                                                                                                                                                                                    a mixture of of human
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specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the E6 protei of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein
                                                                                                                                                                                        ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, specification describes human papillomavirus E6 and E7 polypeptides,
                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMHP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 protein;
                                                                                                                                                                                                                                                                                                                Page 84-85; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of the E6 polypeptide of HPV58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
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Pred. No. 2.3e-47
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RESULT 61
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The invention relates to an antibody composition comprising a mixture of monoclonal antibodies that specifically bind to 86 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to 86 proteins of at least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV 86 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HPV 86 protein in a sample, a method of detecting the presence of an oncogenic HPV 86 protein in a sample and a system for detecting the presence of an oncogenic HPV 86 protein in a sample and a system for detecting the presence of an oncogenic HPV 86 polypeptide in a sample (comprising a first and a second binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the 86 proteins of at least three different oncogenic HPV strains). The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                      New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.
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                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 15; 161pp; English
                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-457781/46
                                                                                                                                                                                                                                                                                                                                                                                            Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2005142541-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPV (oncogenic strain) E6 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LNKRFHNÍSGRWTGRCAVCWRP--RRRQTQV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 496; DB
Pred. No. 3.9e-
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6
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RESULT 62
AEC98870
ID AEC98
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Best Local S
Matches 93
The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
                                                               New polynucleotide comprises a multi-epitope construct comprising nuacids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      composition, kit, methods, and system are useful for diagnosing particularly cervical cancer. The present sequence is an HPV E6
                                                                                                              WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                            03-JAN-2005; 2005WO-US000077
                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 58
                                            Example 10; Page 349; 518pp; English
                                                                                                                                                                                                            (MOTH/)
(BAKE/)
(SOUT/)
(BABE/)
                                                                                                                                                                                                                                                                                                             31-DEC-2003; 2003US-0533211P.
02-JUL-2004; 2004US-0584652P.
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                                                                                                                                                                                                 (CHEN/)
                                                                                                                                                                  (POWE/)
                                                                                                                                                                                                                                                                    (CHES/)
                                                                                                                                                                                                                                                                                         (EPIM-)
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                                                                                                                        Deyoung I
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                                                                                                                                                               MOTHE B.
BAKER D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
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                                                                                                                                                                                                                                                       NEWMAN M J.
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CHESNUT R.
                                                                                                                                                                                                                                                                                         EPIMMUNE INC.
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                                                                                                                                             Newman MJ,
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                                                                                                                                  Mothe B, uang MTF,
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Pred. No. 3.9e-47;
0; Mismatches 36
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                                                                                                                                  Baker
Power
                                                                                                                                  SD,
                                                                                                                                             Southwood
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RESULT 63
AEC96435
ID AEC96435
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KW Humar
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A (CHEX)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the coll CC (comprising the polynucleotide, vector or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the El, E2, E6 and E7 proteins. The CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the CC epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or collipse is useful in preparing a composition for inducing an immune CC epitopes against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition for inducing an immune composition in the claims of the preparing virus (HPV) and thus providing a composition for inducing an immune composition in the claims of the preparing virus (HPV) and thus providing and the providing ar
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Best Local S
Matches 93
                                                                                                                                                                                                                       (EPIM-)
(INNO-)
(CHES/)
                                                                                                                                                                                                                                                                                                                        31-DEC-2003;
02-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPV protein E6 from HPV58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005089164-A2
     (HUAN/)
                                                   (DEYO,
                                                                          (CHEN/
                                                                                                                        (BAKE/
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                                                                                                   BABE/
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MOTHE B.
BAKER D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
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                                                                                                                                                                                                NEWMAN M J.
                                                                                                                                                                                                                            CHESNUT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFQDAEEKPRTLHDLCQALETSVHEIELKCVECKKTLQRSEVYDFVFADLRIVYRDGNFF
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                                                                                                                                                                                                                                                                                                                        2003US-0533211P.
2004US-0584652P.
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Pred. No. 3.9e-47;
0; Mismatches 36
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RESULT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence cc encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the CC inthe crime of HPV and are from the E1. E2, E6 and E7 proteins. The cpitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune CC polypeptide is useful in preparing a composition for inducing an immune CC esponse against human papillomavirus virus (HPV) and thus providing a defense against HPV infection and HPV-related cancers. The present CC invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                       Human papillomavirus type 52
                                                                                                                                                          E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract canc
                                                                                                                                                                                                                                                                                                                     ADO44081 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chesnut R, Newman M. Chen Y, Deyoung LM,
02-OCT-2003; 2003WO-US031726.
                                   15-APR-2004
                                                                                                                                                                                                                Amino acid
                                                                                                                                                                                                                                                 15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                          cancer; reproductive system cancer; penile cancer; vulvar cancer
                                                                                                                                                                                                                                                                                                                                                                                                            121 LNKRFHNISGRWTGRCAVCWRP--RRRQTQV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
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                                                                                                                                                                                                            sequence of the E6 polypeptide of HPV52.
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                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                   protein; 148
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M, Huang MTF,
                                                                                                                                                                                                                                               entry)
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Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
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RESULT 65
AEA98536
THE REPORT OF THE PROPERTY OF 
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, and cancer, and other cancers of the reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
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                                                                                         23-DEC-2004; 2004US-00021949.
                                                                                                                                                                                                                                                                               Human papillomavirus; strain 52
                                                                                                                                                                                                                                                                                                                                              cancer; cervix tumor; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                Papillomavirus infection; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV (oncogenic strain) E6 amino acid sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEA98536 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system, including penile and vulvar cancer.
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                             23-DEC-2003; 2003US-0532373P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 487; DB 8;
; Pred. No. 3.9e-46;
19; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
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В
                                                                                                                                                                                                                                                                                                                                                                                protein; diagnosis; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 polypeptides, (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
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RESULT 66
AEC98868
ID AEC98
XX AEC98
XX O1-DE
XX HUMMAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC monoclonal antibodies that specifically binds to E6 proteins of human C papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC classification with the composition above), a method of detecting an HPV E6 polypeptide in a sample, a method of detecting the presence of an CC comprising the antibody composition above), a method of detecting the presence of an CC concogenic HPV E6 protein in a sample and a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide. CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
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Best Local S
Matches 87
                                                         31-DEC-2003; 2003US-0533211P
02-JUL-2004; 2004US-0584652P
                                                                                                                                              03-JAN-2005; 2005WO-US000077
                                                                                                                                                                                                                                                                                                                                                                               Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEC98868 standard;
                                                                                                                                                                                                                                                               WO2005089164-A2
                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV_52 Envelope protein E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEC98868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lu PS,
   (EPIM-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARBO-) ARBOR VITA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μ
      EPIMMUNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANKRFHNIMGRWTGRCSECWR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKORFHNIRGRWTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFEDPATRPRTLHELCEVLEESVHEIRLQCVQCKKELQRREVYKFLFTDLRIVYRDNNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Belmares MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an antibody composition comprising
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human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 487; DB 9;
Pred. No. 3.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mixture of monoclonal antibodies oma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schweizer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>..</u>
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RESULT 67 AEC96424

AEC96424 standard; protein;

148

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01-DEC-2005

(first entry)

HPV protein

E6 from HPV52

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KKORFHNIRGRWTGRCMSCCR 141

120

61 61 121 121

ANKRFHNIMGRWTGRCSECWR

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                                                                                                                                                      CC (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E3.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence cc encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell cc polynucleotide, vector or polypeptide and a carrier), a cell cc immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from the fifterent strains of HPV and are from the E1, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide in the tables referred to compressive them as papillomavirus virus (HPV) and thus providing a composition for inducing an immune cresponse against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition for inducing an immune cresponse against human papillomavirus virus (HPV) and thus providing a composition for inducing an immune cresponse against human papillomavirus virus (HPV) and thus providing a composition for inducing an immune creation.
                                                                           Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chesnut R, New Y, Deyoung LM,
                                                                                                                                                    Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INNO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOTH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new polynucleotide comprising a multi-epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POWE/)
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                   1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
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CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOTHE B.
BAKER D.
SOUTHWOOD S.
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHESNUT R.
NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INNOGENETICS
MFEDPATRPRTLHELCEVLEESVHEIRLQCVQCKKELQRREVYKFLFTDLRIVYRDNNPY
                                                                             Conservative
                                                                                                                                                    AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ,
                                                                           58.7%; Score 487; DB 9; 61.7%; Pred. No. 3.9e-46; vative 19; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
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Power SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Southwood S,
                                                                                                             Length 148;
                                                                             Indels
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                                                                           0,
                                                                           Gaps
 60
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Matches
                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                               multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chesnut
Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                                                                                                              Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 64; 518pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BAKE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2005; 2005WO-US000077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEYO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /HIOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEWM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHES/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POWE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEN/
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61
                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR, Newsong LM,
                                                                                                                                                                                              1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEYOUNG L M. HUANG M T F. POWER S D.
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BABE L M.
CHEN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOTHE B.
BAKER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEWMAN M J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIMMUNE INC. INNOGENETICS
                                    AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
                                                                                             MFEDPATRPRTLHELCEVLEESVHEIRLQCVQCKKELQRREVYKFLFTDLRIVYRDNNPY
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                                                                                                                                                                                              Conservative
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2004US-0584652P.
                                                                                                                                                                                                                     58.7%;
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                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                           Score 487; DB 9;
Pred. No. 3.9e-46;
9; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker
Power
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                                                                                                                                                                                              35;
                                                                                                                                                                                                                                          Length 148;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
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RESULT 68
AEA98878
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                                                                                                                                                                                                                                                                                     CC monoclonal antibodies that specifically bind to E6 proteins of human C papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an CC oncogenic HPV E6 protein in a sample and a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide. CC where the first binding partner is a PDZ domain protein and the second composition, kit, methods, that specifically binds to the E6 proteins of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                          Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 359; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus; strain 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papillomavirus infection; virucide; E6 protein; diagnosis; antibody; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPV (oncogenic strain) E6 amino acid sequence SEQ ID 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEA98878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEA98878 standard; protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARBO-) ARBOR VITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 121 ANKREHNIMGRWTGRCSECWR
                   122
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                                                   63
                                                                                     62
                                                                                                                                                                                        87;
                                                                                                                      w
                                                                                                                                                      2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garman JD,
KQRFHNIRGRWTGRCMSCCRSSRT
                                                VCQPCLLFYSKVRQYRRYNQSVYGRTLENLTNKQLCNILIRCGKCQKPLCPLEKQRHVDE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKORFHNIRGRWTGRCMSCCR 141
                                                                       VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                  FUNDEERPYKLPALCEBVNISIHBIELDCVYCERQLYRCEVYDFIFRDLCVVYRKGKPLG
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belmares MP,
                                                                                                                                                                                                      58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an antibody composition comprising
                                                                                                                                                                                        17;
                                                                                                                                                                                                      Score 484; DB 9;
Pred. No. 8.4e-46;
                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schweizer J;
                                                                                                                                                                                                                        Length 148;
                                                                                                                                                                                          Indels
                                                                                                                                                                                      ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a mixture
                                                                                                                                                                                      Gaps
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123 NKRFHQIADQWTGRCTQCWRPSAT 146

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                                                                                                                                                                                                                                                                     The invention relates to an antibody composition comprising a mixture of compositional antibodies that specifically bind to E6 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to E6 proteins of at consistent three different oncogenic HPV strains. Also included are a composition that the antibody composition above), a method of detecting an HPV E6 polypeptide in a sample, composition that a sample, a method of detecting the presence of an oncogenic HPV E6 polypeptide in a sample (concogenic HPV E6 polypeptide in a sample (comprising the presence of an oncogenic HPV E6 polypeptide in a sample (comprising the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second composition, kit, methods, and system are useful for diagnosing cancer, composition, kit, methods, and system are useful for diagnosing cancer, composition and cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                 Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                           Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-457781/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus; strain 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papillomavirus cancer; cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV (oncogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEA98538 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-2004; 2004US-00021949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 19; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARBO-)
122
                             121
                                                          62
                                                                                       61
                                                                                                                       N
                                                                                                                                      1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                    , 68
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARBOR VITA CORP
                                                                                    AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                      KKORFHNIRGRWTGRCMSCCRSSRT 145
                                                          GVCQPCLKFYSKIREYRRYRQSVYGTTLENLTNKQLCNILIRCGKCQKPLCPLEKQKHVD
                                                                                                                    EKKRFHQIAEQWTGRCTRCWRPSAT 146
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                               $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; virucide; E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Belmares MP, Somoza DC,
                                                                                                                                                                                                58.2%; Score 483; DB 9; 61.4%; Pred. No. 1.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E6 amino acid
                                                                                                                                                                                 16;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; diagnosis;
                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schweizer
                                                                                                                                                                                                                Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID 19
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody;
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                                                                                                                                                                                                                                                                                                                       E6 proteins
                                                                                                                                                                                    Gaps
                                                           121
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                             ADO44085
ID ADO4
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15-JUL-2004 ADO44085;

(first entry)

RESULT 71

ADO44085 standard; protein; 158

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RESULT 70
AAR97563
ID AAR97763
AC AAR977
AC AAR97
AC AVA:
CC ALIC:
CC AUG:
CC AUG:
CC AUG:
CC AUG:
CARPO7563
AAR975A
AR976A
AR9
                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 molety fused to a full length E7 molety. The variant optionally has a linkage molety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a fusion protein of the C-terminal end of E7 and the N-terminal end of E6. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2003
11-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                    Seguence 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 18; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT31835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edwards SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papilloma virus E6/E7 protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-309518/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9619496-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND.
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                                                                                                                        77
                                                                                                                                                                                                                                                6;
                                                                                                                                                     1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDPAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; cellular
                                                                                                                                                                                                                                                                             Similarity
                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYN 93
                                                                                                                        MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 136
AVCDKCLKFYSKISEYRHYCYSLYGTTLRSHHH 169
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                                                                                                                                                                                                                             57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA,
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                                                                                                                                                                                                                                            Score 478; DB 2;
Pred. No. 4.8e-45;
3; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; vaccine
                                                                                                                                                                                                                                                                                                          Length 172;
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                   Gaps
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RESULT 72
AEA98880
ID AEA98
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AC AEA98
XX
DT 08-SE
XX
DE HPV
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                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
HPV (oncogenic strain) E6 amino acid sequence SEQ ID 361.
                                  08-SEP-2005
                                                                  AEA98880
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                               AEA98880 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 85-86; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002; 2002US-0415929F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-316328/29
                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                TKRRLHKIAGNFTGQCRHCWTSKREDRRRIRQETQV 158
                                                                                                                                                                                                                                                                                                                              MFQDPQERPKKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                               KKORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                            ACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYNLLIRCMSCLKPLCPAEKLRHLT
                                                                                                                                                                                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                             LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFSDLCVVYRDGVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               56.4%;
55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the
                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EG
                                                                                                                                                                                                                                                                                                                                                                                          Score 468.5; DB Pred. No. 5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide of HPV68
                                                                                                 ⋛
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E7 polypeptides, (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                              158;
                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                              62
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SEXSEEXEX

27-AUG-2003 11-JAN-1997

(revised) (first entry)

AAR97562

standard; protein;

172

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Human papilloma virus E6/E7 protein variant.

片 S 밁 ঠ 밁 Ś

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RESULT 73
AAR97562
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic kit (for detecting an HPV E6 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second binding partner is a PDZ domain binds to the E6 protein of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least of the monoclonal antibodies specifically binds to E6 proteins of at least three different oncogenic HPV strains. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an monoclonal antibodies that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 361; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2005142541-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus; strain 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ARBO-) ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2005
                                                                                                                                                                     122
                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                         2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garman JD,
                                                                                                                                                                                                                              ACOKCIKFHAKVRELRHYSNSVYATTLESITNTKLYNLSIRCMSCLKPLCPAEKLRHVNT 123
                                                                                                             KRRFHQIAGSYTGQCRHCWTSNREDRRRIRRETQV
                                                                                                                                                                KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                                                                                                                      FPNPAERPYKLPDLCTALDTTLHDITIDCVYCKTQLQQTEVYEFAFSDLFIVYRNGEPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Belmares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically bind to E6 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 468.5; DB 9;
Pred. No. 5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΜÞ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      where at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a mixture of of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E6 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPV
                                                                                                                                                                                                                                                                                                                                           63
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RESULT 74
AD044080
ID AD044
XX AD044
XX AD044
XX AD044
XX AD046
XX AMinc
XX AMinc
XX Cervi
KW E6 pr
KW Cervi
KW anal
XX AUMAR
OS Humar
XX MO200
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a delection mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This is a fusion protein of the C-terminal end of E6 and the N-terminal end of E7. The protein is also a deletion mutant generated from the sequence described in AAT31833. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papilloma virus; E6; humoral immune response; ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ( UYQU )
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 17; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine variants of human p
E6 and/or E7 protein, pref.
prevent HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-309518/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9619496-A1
                                                                     E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                        15-JUL-2004
                                          Human papillomavirus
                                                                                                                            Amino acid
                                                                                                                                                                                                              ADO44080 standard; protein; 151
                                                                                                                                                                                                                                                                                                       111 CPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                   87;
                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                           2
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UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT31834
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                         CPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cox J,
                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94AU-00000157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-AU000868
                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                               56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Webb
                                         type 51
                                                                                                                             of the E6 polypeptide of HPV51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; E7; deletion mutant; HPV; immune response; cellular immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               papilloma virus antigens - contain variants of f. deletion mutants, and are used to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ę
                                                                                                                                                                                                                                                                                                                                                                                                Score 468; DB 2;
Pred. No. 6.3e-44;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frazer I;
                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                          110
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RESULT 75
AEA98543
ID AEA98
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                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AD044074-AD044085 represent E6 polypeptides from human papillomaviruses. CC AD044098 is the consensus sequence derived from these polypeptides. The CG specification describes human papillomavirus E6 and E7 polypeptides. CC where the E7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in CC AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there is sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated CC cancers, such as cervical cancer. The fusion proteins are useful for generating immune responses CC encoding the fusion proteins are useful for generating immune responses CC against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
 PFX BXX SXX XXX BXX XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 82; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADO44107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                   Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.
23-DEC-2004; 2004US-00021949
                             30-JUN-2005
                                                           US2005142541-A1
                                                                                                                                                                 HPV (oncogenic
                                                                                                                                                                                              08-SEP-2005
                                                                                                                                                                                                                                                          AEA98543 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-316328/29.
                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                       papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKORFHNIRGRWTGRCMSCCRSSRTRRETOL
                                                                                                                                                                                                                                                                                                                                                                                                                      AVXDKCTKEYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cassetti
                                                                                                                                                                                                                                                                                                                                   EKKRFHEÍAGRWTGQCANCWQRTRQRNETQV
                                                                                                                                                                                                                                                                                                                                                                                             AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEBKQKLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                              (first entry)
                                                                                                                                                                 strain) E6 amino acid sequence SEQ ID 24.
                                                                                                                                                                                                                                                          protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%;
                                                                                         strain 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 460; DB 8;
Pred. No. 4.2e-43;
                                                                                                                                      E)
                                                                                                                                      protein; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E7 polypeptides, (HPV)-associated
                                                                                                                                         antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
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ARESULT 76
AD044079
ID AD044
XX AD044
XX AD044
XX AD15-JU
DE Amino
XX E6 pr
KW cervi
KW anal
XX AD040
XX Human
XX W0200
PD 15-AP
PX Y2-OC
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to 86 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to 86 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV 86 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC Ed protein in a sample, a method of detecting the presence of an CC oncogenic HPV 86 protein in a sample for detecting the CC presence of an oncogenic HPV 86 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV Ed polypeptide, CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the 86 proteins CC of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
             02-OCT-2003; 2003WO-US031726
                                             15-APR-2004.
                                                                                                     Human papillomavirus type
                                                                                                                                                   cervical cancer;
                                                                                                                                                              E6 protein;
                                                                                                                                                                                             Amino acid
                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                     ADO44079;
                                                                                                                                                                                                                                                                                 ADO44079 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 24; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ę
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ARBO-)
                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2005-457781/46
                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                         EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
                                                                                                                                                                                                                                                                                                                                                                                                                       AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEEKQKLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                          sequence of the E6 polypeptide of HPV45.
                                                                                                                                                            E7 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                             E7 protein; fusion protein; HPV; HPV-associated cancer; cer; immune response; lower gastrointestinal tract cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belmares MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.4%; Score 460; DB 9; 57.0%; Pred. No. 4.2e-43; tive 24; Mismatches 41
                                                                                                      45
                                                                                                                                                                                                                                                                                   158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                         RESULT 77
AEA98548
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Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.

1 1 1

protein; diagnosis; antibody;

HPV (oncogenic strain) E6 amino acid sequence SEQ ID

08-SEP-2005 AEA98548;

(first entry)

AEA98548

standard; protein; 158

Human papillomavirus;

strain 45

(ARBO-) ARBOR VITA CORP 23-DEC-2003; 2003US-0532373P 23-DEC-2004; 30-JUN-2005 US2005142541-A1

2004US-00021949

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                                                                                                                                                                                                                                                                                AD044074-AD044085 represent E6 polypeptides from human papillomaviruses.

AD044098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides. The where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                       tract cancers, e.g
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 81-82; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMHP ) WYETH HOLDINGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-316328/29
                                  122
124
                                                                    64 ACHKCIDFYSRİRELRYYSNSVYGETLEKITNTELYNLLİRCLRCQKPLNPAEKRRHLKD 123
                                                                                                       62
                                                                                                                                                                                                             87;
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                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                158
                                                                                        VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                            FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                         FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
KRRFHSIAGQYRGQCNTCCDQARQERLRRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cassetti
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                ß,
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                                                                                                                                                                                                                           56.1%;
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                                                                                                                                                                                                             22;
                                                                                                                                                                                                           Score 459.5; DB 8
Pred. No. 5.1e-43;
2; Mismatches 41
                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                             41;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                               158;
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RESULT 78
AEC98867
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV E6 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is a perfically binds to the E6 proteins of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibodies that specifically bind to E6 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least of the monoclonal antibodies specifically binds to E6 proteins of at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ę
                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                     Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                    01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                               AEC98867 standard; protein; 158
                                            31-DEC-2003; 2003US-0533211P
02-JUL-2004; 2004US-0584652P
                                                                                          03-JAN-2005; 2005WO-US000077
(INNO-) INNOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an antibody composition comprising a mixture of oclonal antibodies that specifically bind to E6 proteins of human illoma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncogenic
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                                                                                                                                                                                                                                                                   Envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACHKCIDFYSRIRELRYYSNSVYGETLEKITNTELYNLLIRCLRCQKPLNPAEKRRHLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FODPOERPRKLPOLCTELOTTIHDIILECVYCKOOLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                           KRRFHSIAGOYRGOCNTCCDQARQERLRRRETOV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDDPKQRPYKLPDLCTELNTSLQDVSIACVÝCKATLERTEVÝQFAFKDLCIVÝRDCIAÝA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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c strains of
                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                   protein E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.4%; Score 459.5; DB 9
56.1%; Pred. No. 5.1e-43;
tive 22; Mismatches 41
 ş
                                                                                                                                                                                       type 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising a mixture of human papilloma virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of monoclonal
s, useful for (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l antibodies
diagnosing
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AAR63866 ID AAR

AAR63866 standard;

protein; 158

RESULT 79

SARPRAX

16-OCT-2003 25-MAR-2003

(revised)

(first entry)

AAR63866;

28-JUN-1995 HPV18 E6/E7

proteins

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                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence cc encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the CC comprising the polynucleotide, vector or polypeptide, inducing an CC immune response against human papillomavirus virus (HPV) and making the CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the cepitopes may be linked via a GP-anchor/spacer peptide. The order of the cc claims of the specification. The polynucleotide, vector or polypeptide in the tables referred to in the claims of the specification. The polynucleotide, vector or composition for inducing an immune cc response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition for inducing an immune componse against human papillomavirus virus (HPV) and thus providing a component of the present of t
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHES/)
(NEWM/)
(MOTH/)
(BAKE/)
(SOUT/)
                                                                                                                                                                                                                                                                                                                                                Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-658982/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BABE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEN/
                                                                                                                                                                                                                                                                                  Local Similarity
                                         122 KORFHNIRGRWTGRCMSCCRSS----RTRRETOL 151
                                                                                      64 ACHKCIDFYSRIRELRYYSNSVYGETLEKITNTELYNLLIRCLRCOKPLNPAEKRRHLKD
                                                                                                                                                                                                                                                                87;
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HUANG M T F.
POWER S D.
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NEWMAN M J.
MOTHE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Newman MJ,
Deyoung LM,
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CHEN Y.
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BABE L M.
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                                                                                                                         VXDKCLKFYSKISEYRHYCYSYYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                           FDDPKQRPYKLPDLCTELNTSLQDVSIACVÝCKATLERTEVÝQFAFKDLCIVÝRDCIAÝA
                                                                                                                                                                                                           FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
KRRFHSIAGQYRGQCNTCCDQARQERLRRRETQV
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                    55.4%; Score 459.5; DB 9 56.1%; Pred. No. 5.1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mothe B,
                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                  Mismatches
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Power
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                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                         9:
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RESULT 80
AAR79656
ID AAR79
XX AAR79
XX 25-MA
DT 25-MA
DT 06-DE
XX Ubiqu
KW Cell
XX Cell
XX Ubiqu
KW Cell
XX W0951
XX Homo
XX W0951
XX W13-JU
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences of the E6 and E7 polypeptide-encoding regions of human papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded proteins in AAR63865-66, respectively. Probes and primers based on these sequences were used for HPV infection diagnosis; expression of E6 and E7 is diagnostic for cervical cancer or pre-mallgnant states. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
            13-JUL-1995
                                                                             Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell proliferation; cancer; psoriasis; fibrosis.
                                                                                                                   HPV-18
                                                                                                                                       25-MAR-2003
06-DEC-1995
                                                                                                                                                                                               AAR79656
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27-28; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1993;
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                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                               KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                      ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
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                                                                                                                                                                                                                                                                                                                                                                   FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 455.5; DB 2
56.1%; Pred. No. 1.4e-42;
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23-MAY-1994;
27-MAY-1994;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                  Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis; cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis; prolliferative disorder; cancer; restenosis; tissue connective disorder; wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma; insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA library using the primers given in AAQ97846-47. The gene was subcloned into a baculovirus vector for expression of recombinant E6 in Sf9 insect cells for use as a component of an in vitro ubiquitin conjugating system. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating e.g. cell proliferation.
04-JAN-1994;
23-MAY-1994;
                                                                                                                                                                                                                                                                                            diagnosis; therapy; E6.
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                                                                                                            HPV-18 E6; ubiquitin mediated proteolysis; human; cellular protein half life; ubiquitination inhibitor; p53; cyclin; cell cycle regulator; myc deregulation; human papillomavirus; cell cycle regulator; myc deregulation; human papillomavirus; HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia; epidermal neoplasia; psoriasis; connective tissue disorder; wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cirrhosis, and scleroderma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human papillomavirus E6 protein. The invention relates to assays for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein comprising contacting a candidate agent with an ubiquitin-conjugating system and measuring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-590402/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1994;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                      HPV-18
                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003
23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying ubiquitination inhibitors using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITO-)
   US6068982-A
                                                      Human papillomavirus; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB03176 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB03176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
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                                                                                                                                                                                                                                                                                                                      E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORFHNIRGRWTGRCMSCCRSSR----TRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cottarel G,
                                                                                                                                                                                                                                                                                                                      protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00250795.
94US-00305520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 455.5; DB 2
Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel ubiquitin conjugating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draetta G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158;
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64

ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE

151

VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121 FEDETRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA

4

122 KQRFHNIRGRWTGRCMSCCRSSR-----TRRETQL

KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV

Query Match Best Local S Matches 87

Similarity

54.9%;

Score 455.5; DB 3 Pred. No. 1.4e-42;

DB 3;

Length 158; Indels

87;

Conservative

21;

Mismatches

42;

<u>ა</u>

63

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cu ubiquitin-mediated proteolysis of a cell cycle regulatory protein comprising contacting an engineered eukaryotic cell with a candidate cagent. The eukaryotic cells is engineered to express a recombinant human, candida albicans or Schizosaccharomyces pombe ubiquitin- conjugating companies (AAB03169-B03171), a cell cycle regulatory protein (such as p53) cand schizosaccharomyces pombe ubiquitin- conjugating captures, https://doi.org/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/10.2016/1
  27-MAY-1994;
13-SEP-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory protein for treating cancers involves measuring ubiquitination levels of the protein in the presence of candidate agent in an eukaryotic cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-1994;
23-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of identifying ubiquitin-mediated proteolysis of a cell cycle re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Col 97-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (-OTIM)
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  158
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94US-00247904.
94US-00250795.
94US-00305520.
95US-00486663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin
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RESULT 83
AAB98427
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                                                                                    S
                                                                                                                                                                                              treatment or prophylaxis of HPV infection, in persons who have not can manifested symptoms e.g. genital warts or neoplastic growth. The peptides can also be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen, and as reagents to evaluate immune recall responses or evaluate the efficacy of a vaccine. The vaccine compositions are useful for removing warts or treating HPV infections. The epitopes for inclusion in an epitope-base vaccine may be selected from conserved regions of viral or tumour-associated antigens, which reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-base vaccines. An additional advantage is the ability to combine selected epitopes (CTL and HTL) and to modify the composition of the epitopes achieving enhanced immunogenicity, the major benefit of the vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
                                                                                                                                           Query Match
Best Local :
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antivital activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the present invention are useful for stimulating an immune response to HPV by stimulating the production of CTL or HTL responses, specifically in the
                                                                                                                                                                                              Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 22; 756pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated human papilloma virus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-381497/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1999; 99US-0172705P.
15-AUG-2000; 2000US-00641528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart; neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus protein HPV18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-2000; 2000WO-US033549.
                      62
                                                       4
                                                                                                                         l Similarity
87; Conser
VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                     FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                    FODPOERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sidney J,
                                                                                                                         Conservative
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                                                                                                                                         54.9%; Score 455.5; DB 4; 56.1%; Pred. No. 1.4e-42;
                                                                                                                         21;
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                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope, useful in vaccines
                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celis
                                                                                                                         Indels
                                                                                                                                                        Length 158;
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                                                                                                                         5.
                                                                                                                       Gaps
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62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEBKQRHLDK 121

ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE

FEDPTRRPYKLPDLCTELNTSLQD1E1TCVYCKTVLELTEVFEFAFKDLFVVYRDS1PHA

64

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Query Match Best Local S Matches 87

1 Similarity 87; Conserv

54.9%; ilarity 56.1%; Conservative 2

21;

Score 455.5; DB 8; Pred. No. 1.4e-42; 1; Mismatches 42;

Indels Length

Gaps

61 63

158; S

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                               ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV) -associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer, anal cancer; reproductive system cancer; penile cancer; vulvar cancer
Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 78; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO44074 standard; protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of the E6
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124 KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158

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RESULT 85
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                                                                                                                                                                                                                                                                            The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E5 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample for detecting the CC presence of an oncogenic HPV E6 protein a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody the specifically binds to the E6 proteins of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                    Matches
                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                  Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibody composition for oncogenic strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu PS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPV (oncogenic strain) E6 amino acid sequence SEQ ID 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 28; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oncogenic
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122 KQRFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                    64
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                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQRFHNIRGRWTGRCMSCCRSSR----TRRETQL
                                                                                 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                    ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                    FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                   FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; virucide; E6 protein; diagnosis; antibody;
                                                                                                                                                                                                  56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belmares MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a mixture of monoclonal antibodies human papilloma virus, useful for diagnosing
                                                                                                                                                                                    21;
                                                                                                                                                                                                  Score 455.5; DB 9
Pred. No. 1.4e-42;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Somoza DC,
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                                                                                                                                                                                    Gaps
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RESULT 86
AEBIL193
ID AEBIL
XX AEBIL
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a synthetic protein of a pathogen or tumor comprises chemically synthesizing two or more fragments of 2-80 contiguous amino acids of sequence, the sequence of two or more fragments are neighboring and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-2003; 2003WO-NL000929.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYLE-) UNIV LEIDEN MEDICAL CENT.
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   64
                                                                   62
                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                             Similarity
ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                               VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                      FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                          54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53pp; English
                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                      Score 455.5; DB 9
Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                          Length 158;
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                   multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E8 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against HPV infection and HPV-related cancers. The present
                                                                                                                                                                                                         The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16 EB1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2005089164-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPV_18 Envelope
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                                                                                                                                                                                                                                                                                                Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                           New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHEN/)
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02-JUL-2004;
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          sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POWE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNO-)
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                                                                                                                                                                                                                                                                                                                                                          polynucleotide
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HUANG M T F.
POWER S D.
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BAKER D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEWMAN M J.
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RESULT 88
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Best Local Similarity
Matches 87; Conser
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construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                        New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
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02-JUL-2004;
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POWER S D.
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Deyoung LM,
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56.1%; Pred. No. 1.4e-42;
tive 21; Mismatches 42
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RESULT 8s
AAAO22924
ID AAO22924
AC AAO2
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Best Local (
                                                                                                 A new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a highly immunogenic fusion partner is useful to vaccinate against HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                    Disclosure;
                                                                                                                                                                                                                                                                              N-PSDB; AAL53422.
                                                                                                                                                                                                                                                                                                                                                                               Cid-Arregui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus-18 (HPV18) EE6T-protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEKR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                              2002-724952/79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                partner; immunogenicity; HPV inf
papillomavirus-18; EE6T-sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ACHKCIDFYSRIRELRHYSDSYYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEUT KREBSFORSCHUNGSZENTRUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEDETRREYKLEDICTELNTSLODIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; E6; E7 fusion protein; HF rrner: immunogenicity; HPV infection;
                            Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Zur Hausen H;
                                    4.
                            34pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%;
56.1%;
                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
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Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ይ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPV; immunogenic; vaccine;
n; neoplasm; HPV18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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Best Local :
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25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing a mutation which results in production of a truncated non-functional protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV E66T-protein sequence represents the human papillomavirus-18 (HPV18)
                                                            Recombinant virus vectors encoding human papillomavirus proteins - for treating and vaccinating against HPV infections and conditions caused l
                                                                                                  N-PSDB; AAQ29390.
                                                                                                                                                                                         14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                              Human papillomavirus; 18.
                     Disclosure; Fig 1b; 83pp;
                                                chem,
                                                                                                               WPI; 1992-349219/42.
                                                                                                                                       Boursnell MEG,
                                                                                                                                                                                                                                            01-OCT-1992.
                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                     Virus vector;
                                                                                                                                                                                                                                                                                                                                                                                                            HPV 18 E6 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR27728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 172 AA;
                                                                                                                                                                 ( DWMI)
                                                                                                                                                                                                                                                                    WO9216636-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR27728;
                                             reating and vaccinating against them, such as cervical cancer.
                                                                                                                                                                                                                 10-MAR-1992;
                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                        immunotherapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPAEKLRHLNE
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                                                                                                                                                                 IMMUNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQRFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                    vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                         91GB-00005383
                                                                                                                                                                                                                   92WO-GB000424
                                                                                                                                      Inglis SC,
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
2. .259
                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.1%;
                                                                                                                                                                                                                                                                                             "HPV-18 E6 protein"
                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                       Munro
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Pred. No. 1.6e-42;
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The fragment of

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HPV-18

E6/E7

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AAX25385
ID 2A325
XX AX25
XX AX25
XX DT 06-SE
XX Pusic
KW Fusic
KW HPV a
XX Synth
OS Human
XX WO993
XX WO993
XX WO993
XX WO18-DE
XX LSWIF
DD 08-JT
PA (SMIF
PA WPI;
DR W-PSI
DR W-PSI
DR W-PSI
DR W-PSI
DR W-PSI
CC HPV
CC HPV
CC HPV
CC HPV
CX AAX71
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 271 AA;
                                                                                                                   Composition comprising induce immune response
                                                                                                                                                                                                                      Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                         18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                             WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
immunological fusion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY25385 standard;
                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                      1999-405485/34.
DB; AAX78800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
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                                                                                     XI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEDETRREYKLEDICTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein D1/3-E6-His/HPV18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%;
ilarity 56.1%;
Conservative 2
                                                                                 Page 59-60; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                        Gerard
                                                                                                                                                                                                                                                                                           97GB-00027262.
                                                                                                                                                                                                                                                                                                                         98WO-EP008563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              partner;
                                                                                                                    to
                                                                                                                    E6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 455.5; DB 2; Pred. No. 2.7e-42; 21; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                    E7
                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                      or E6/E7
                                                                                                                                      fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                    protein
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AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG

from

Sequence

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                                             This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                            Disclosure; Fig 22; 95pp; English.
                                                                                                                                                                                                                                                                                                                                 Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruck C, Cabezon (
Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1999
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22-JUN-1999
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DB; AAX29789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cabezon Silva
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97GB-00017953
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Pred. No. 2.8e-42;
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                                                                                     The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                             Sequence 278
                                                                                                                                                                                                                                                                                                                   04-MAR-2005
                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 18. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein;
virucide; uteri;
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DB; AED52652.
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FQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KORFHNIRGRWTGRCMSCCRSSR----TRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                 ptein; vaccine; papilloma; cytostatic; papillomavirus
uterine cervix tumor; E6; D protein.
                                                                                                                                                                                                                                                                                                                                                                                influenzae; strain 772
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                            Conservative
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Pred. No. 2.8e-
21; Mismatches
                          Score 455.5; I
Pred. No. 2.8e
21; Mismatches
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                           5; DB 9;
2.8e-42;
hes 42;
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                                          Length
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RESULT 94
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                                                                                                                                                                                                               Query Match
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Matches 87
                                                                                                                                                                                                                                                                                                                    AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonuclectide. The products of the invention can be used to induce arimmune response in a patient to an HPV antigen. They can also be used i preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAH
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                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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immunological fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPV fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               papillomavirus.
                                                                                                                                                                                                                 87;
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                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XII; Page 61-62; 62pp;
                                                                                                                                                                                                                                                                                        383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151 |:||||| : |:| ||| : | |||||: KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 269
                        KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                     ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                           VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK 121
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                                                                                                                                                                FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
                                                                                                                                          FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                             54.9%;
nilarity 56.1%;
Conservative 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-00027262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                 Score 455.5; DB 2
Pred. No. 4.1e-42;
1; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 protein; E6/E7; immunomodulator; tumour; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E7
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RESULT 96
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a chimeric B6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                          AED52657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 25; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Papilloma Virus (HPV) fusion proteins - useful in vaccines treatment or prophylaxis of HPV induced lesions.
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Haemophilus influenza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
22-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                   62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87;
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                                                                                                                                                                                                                                                                                                                                                                                             FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                              FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                      KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                    ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPAEKLRHLNE
                                                                                                                                                                       KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.9%; Score 455.5; DB 2; 56.1%; Pred. No. 4.1e-42; tive 21; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 383;
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standard; protein; 383

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RESULT 97
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                              Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 18. Synthetic.
                                    08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 17; Fig 25; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyrrell AWR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection; virucide; uterine cervix tumor; E7; E6; D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-2005
         HPV (oncogenic strain)
                                                                                      AEA98550
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)B; AED52656.
                                                                                                                                                                                                       175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                           115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein D1/3-E6-E7-Hi8/HPV18
                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                            87; Conserv
                                                                                                                                                    KORFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
|:||||| : |:| ||| :| |||||:
KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 269
                                                                                                                                                                                                                             VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                         FEDPTRRYXLPDLCTELNTSLQDIEITCYYCKTVLELTEVFEFAFKDLFVVYRDSIPHA 174
                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                         54.9%; Score 455.5; DB 9 clarity 56.1%; Pred. No. 4.1e-42; Conservative 21; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                               B
                                    (first entry)
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                                                                                    protein; 162
            о
ы
          amino acid sequence
                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                             42;
            SEQ
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            ╏
                                                                                                                                                                                                                                                                                                                                       . 383;
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RESULT 98
ADL90077
ID ADL90
XX
AC ADL90
XX
AC ADL90
XX
XX
DT 17-JU
XX
XX
KW Immun
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to E6 proteins of at CC diagnostic kit (for detecting an HPV E8 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CE protein in a sample, a method of detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising the concogenic HPV E6 protein and a system for detecting the concogenic HPV E6 protein and a system for detecting an CC first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins of at least three different oncogenic HPV Extrains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 86
                                               Human papillomavirus 18-E6 protein, SEQ ID
                                                                               17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 31; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-457781/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
                  Immune response;
                                                                                                                                              ADL90077 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody composition oncogenic strains of
                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                            96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garman JD,
                                                                                                                                                                                                                                                 | KKQRFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                             MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                              SKRRFHKIAGNFTGOCRHCWTSKREDRRRTROETQV 162
                                                                                                                                                                                                                                                                                             AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
                                                                                                                                                                                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCDEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                             LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                               (first
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                immunoglobulin; Ig; E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belmares
                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%; Score 451.5; DB 9;
55.1%; Pred. No. 4.1e-42;
cive 21; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a mixture of human papilloma virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somoza
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                                                  17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of monoclonal antibodies s, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
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                                                                                                                                                                                                                                                                                                126
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03-OCT-2002; 2002US-0415929P 02-OCT-2003; 2003WO-US031726

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RESULT 99
AD044078
ID AD044
XX AD044
XX AD044
XX AMinc
XX B6 Minc
XX E6 Minc
XX B6 W Cervi
XX anal
XX WO200
XX WO200
YX WO200
YX O2-00
YR O3-00
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen sequence, used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                             E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract canc
                                                                                                                                                                                                                                                                                                                                                        ADO44078 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1G; 154pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-2002;
14-MAR-2003;
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                                                                                                                                                                                                                                                                                                                     ADO44078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ASTR-)
                                                                                                                                        Human papillomavirus
                                                                                                                                                                                                                                                Amino acid
                                                                                                                                                                                                                                                                                   15-JUL-2004
                                                                       15-APR-2004
                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASTRAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                             KRRFHKIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEDPTRRPYKLPDLCTELNTSLQDIEITCVÝCKTVLELTEVFEPAFKDLFVVÝRDSIPHA
                                                                                                                                                                                                                                              sequence of the E6
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2003WO-US007995
                                                                                                                                                                             reproductive system cancer;
                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.2%;
                                                                                                                                          type 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 449.5; DB 8; ; Pred. No. 6.7e-42; 21; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips
                                                                                                                                                                                                                                                                                                                                                        158
                                                                                                                                                                                                                                                polypeptide of
                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                           penile
                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for generating immunoglobulin
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د.
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RESULT 100
ADV85646
ID ADV856
XX ADV856
XX ADV856
XX Human
XX Cytost
KW Cytost
KW Cancer
XX Human
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
XX US2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD044074-AD044085 represent E6 polypeptides from human papillomaviruses. AD044098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides. The where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 86
 31-JAN-1995;
31-JAN-1996;
05-JUN-2000;
09-AUG-2001;
                                                                                                                                                                                                                                                                  Cytostatic; Virucide; Antibacterial; Antiparasitic; Vaccine; infection;
                                                                                                                                                                                                                                                                                                   Human papillomavirus E6 protein, SEQ ID
                                                                                            12-MAR-2004;
                                                                                                                                                                                                         Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                             10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                  ADV85646;
                                                                                                                                                                                                                                                                                                                                                                                                                    ADV85646 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                       US2004258688-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 80-81; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KQRFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ACQSCIKFYAKIRELRYYSDSVYATTLENITNTKLYNLLIRCMCCLKPLCPAEKLRHLNS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRRFHKIAGSYTGQCRRCWTTKREDRRLTRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.2%; Score 449.5; DB 8; ilarity 55.5%; Pred. No. 6.7e-42; Conservative 19; Mismatches 45;
 95US-00381528.
96WO-US001383.
2000US-00586704.
2001US-00925284.
                                                                                              2004US-00800023
                                                                                                                                                                                                                                                                                                                                             (first entry
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                                                                                                                                                                                                                                                                                                       27.
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Search completed: May 27, Job time: 359.727 secs

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                                                                                                                                                                                                                                                                                                                          CC mammal to either: a conjugate comprising a preselected antigen covalently CC bound to an antibody to DEC-205; or a recombinant anti-DEC-205 antibody CC genetically engineered to contain at least one preselected antigen on at CC least one preselected site on the antibody molecule; and promoting CC antibody (fragment) is preferably selected from ADV85632 and ADV85633, CC which encode the heavy or light chain variable region of an anti-DEC-205 CC antibody. The antigen is targeted to antigen presenting cells through the CC inclusion of the anti-DEC-205 antibody, The anti-DEC-205 antibody, The inmunity induced is robust and long lasting, even CC from a single dose at low concentration. The method of the invention is CC used an anti-DEC-205 a mammal to prevent or treat a disease such as a CC viral, bacterial or other infection or cancer. The immunization and CC immunity. The present sequence is a HPV protein sequence which can be CC used as a variance anticen.
                                                                                                                                                                                                                                          Best Local Similarity
Matches 86; Conser
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method (M1) for promoting highly efficient antigen presentation in a mammal, by targeting a preselected antigen to an endocytic receptor on an antigen-presenting cell, e.g. a dendritic cell. An example of a dendritic cell is the cell endocytic receptor DEC-205. The method comprises exposing dendritic cells from the
                                                                                                                                                                                                                                                                                                                     Sequence 158 AA;
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(NUSS/)
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124
                                   122 KORFHNIRGRWTGRCMSCCRSSR----TRRETOL 151
                                                                             64 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                      62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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                                                                                                                                                                                 2 FQDPQERPRKLPQICTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
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NUSSENZWEIG M
STEINMAN R M.
                                                                                                                                                                                                                                                                                                                                                           a vaccine antigen.
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KRRFHKIAGHYRGQCHSCCNRARQERLQRRRETQV
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C;Sperio
                                                                                                                                                                                                                        A;Note: host Homo sapiens (man)

G;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

G;Accession: E40824; S36521

R,Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A;Title: The phylogenetic relationship and complete nucleotide sequence of A;Reference number: A40824; MUID:92124753; PMID:1310198

A;Accession: E40824
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C;Superf
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A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Residues: 1-158 <SEE>
                       A; Reference number: S36469
A; Accession: S36521
                                                                                          A;Cross-references: UNIPROT:P27228; UNIPARC:UPI R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein - human papillomavirus type C;Species: human papillomavirus type 35
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C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
                                                                     A; Description: Primer-directed sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: A negative element in the human poapillomavirus A;Reference number: Z17014; MUID:91162763; PMID:1848319 A;Accession: T10427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-158 < KEN>
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  Statue:
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Pred. No. 2.7e-71;
1; Mismatches 2;
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E6 protein - human papillomavirus C;Species: human papillomavirus ty C;Bate: 30-Jun-1987 #sequence_revi C;Bate: 30-Jun-1986 #sequence_revi C;Accession: A03683 R;Cole, S.T.; Streeck, R.E. J. Virol. 58, 991-995, 1986

#sequence_revision

30-Jun-1987 #text_change 09-Jul-2004

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A; Title: Genome

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A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
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A; Residues: 1-149 <GOL>
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A;Title: Nucleotide sequence of human papillomavirus type 31:
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Goldsborough, M.D.; DiSilvestre,
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                                                                                                                                                                                                                                            , 86
                                                                                                                                                                                           1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                GVCTKCLRFYSKVSEFRWYRYSVYGTTLEKLTNKGICDLLIRCITCQRPLCPEEKQRHLD
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                                     KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                              MFKNPAERPRKLHELSSALEIPYDELRLNCVYCKGQLTETEVLDFAFTDLTIVYRDDTPH
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KKKRFHNIGGRWTGRCIACWR--RPRTETQV 149
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                                                                                                                                                                                                                                                               64.9%;
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                                                                                                                                                                                                                                                            Score 523; DB 1;
Pred. No. 9.9e-43;
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RESULT 6
A61237
E6 protein - human papillomavirus type 52
E6 proteis: human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C;Accession: A61237
R;Takami, Y; Kondoh, G; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, Int. J. Cancer 48, 516-522, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: host Homo sapiens (man)
G;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
G;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
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A;Accession: A03633
A;Molecule type: DNA
A;Residues: 1-149 <COL>
A;Cross-references: UNIPROT:P06427; UNIPARC:UPI00001383CD;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
C;Keywords: DNA binding; early protein; zinc finger
C;Keywords: DNA binding; CCCC motif
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W6WL58
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A;Reference number: A36779; MUID:92024102;
A;Accession: E36779
A;Status: translation not shown
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A; Residues: 1-149 < KIR>
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Species: human papillomavirus type 58
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                                                                                                                                                                                                                                                                                                                       AVCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.8%; Score 496; DB 1; 61.6%; Pred. No. 3.7e-40;
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63.6%; Pred. No. 1.9e-42;
tive 19; Mismatches 34
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; PMID:1656594
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A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA
A;Residues: 1-148

E6 protein - human papillomavirus type 34 C;Speciss: human papillomavirus type 34 C;Date: 20-Feb-1995 #sequence_revision 20 C;Accession: S36515 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August A;Description: Primer_directed sequencing

20-Feb-1995

#text_change

09-Jul-2004

sequencing o

of hu

human

papillomavirus

S36515

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A; Molecule type: DNA
A; Residues: 1-148 <DEL>
A; Residues: 1-148 <DEL>
A; Cross-references: UNIPROT: P36814; UNIPARC: UPI00001383DD;
A; Cross-references: UNIPROT: P36814; UNIPARC: UPI00001383DD;
C; Superfamily: papillomavirus E6 protein; nucleus; zinc finge
C; Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S36573
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing of
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S36573
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A;Residues: 1-148 <TAK>
A;Cross-references: UNIPARC:UPI0000178415
C;Superfamily: papillomavirus E6 protein
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A;Accession: S36573
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Best Local Similarity
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87; Conserv
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                                                   ANKREHNIMGRWTGRCSECWR
                                                                                                                      GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
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                                                                                                                                                                                                                                                                Score 487; DB 2;
Pred. No. 2.6e-39;
9; Mismatches 35;
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Pred. No. 2.6e-39;
9; Mismatches 35
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                                                                                                                                                                                                                                                                                                                                   nucleus; zinc finger
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of human
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E6 protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Ritle: Biologic properties and nucleotide sequence analysis of human papil A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Accession: E40415
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W6WL51
E6 protein - 1
                                                                                            C;Accession: S36561
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing o
                                                                                                                                                     86 protein - human papillomavirus type 45
C;SpecLes: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P26554; UNIPARC:UPI00001383DC; GB:M62877 (C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;30-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
  A;Cross-references: UNIPROT:P21735; UNIPARC:UPI00001383D8; EMBL:X74479; NID:g397022;
                  A; Molecule type: DNA
A; Residues: 1-158 < DEL>
                                                                              A; Reference number: S36469
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                                                            A;Accession: S36561
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Best Local
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                                                                                                                                                                                                                                                                                                              EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
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Pred. No. 5.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 460; DB 1;
Pred. No. 1e-36;
14; Mismatches 41
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                                                                                              st 1993
J of human
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A;Accession: G26251
A;Molecule type: DNA
A;Residues: 1-158 <COL>
A;Residues: 1-158 <COL>
A;Cross-references: UNIPARC:UPI000002C0FB; GB:X05015; NID:g60975; PIDN:CAA28664.1;
A;Cross-references: UNIPARC:UPI000002C0FB; GB:X05015; NID:g60975; PIDN:CAA28664.1;
A;Cross-references: UNIPARC:UPI000002C0FB; GB:X05015; NID:g60975; PIDN:CAA28664.1;
C. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and A;Reference number: A92791; MUID:86306665; PMID:3018129
A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
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C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Nucleotide sequence and comparative analysis of A; Reference number: A92937; MUID:87283882; PMID:3039146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-158 <SEE>
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Matches 87; Conserv
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Best Local
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es 87; Conserv
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                                                     122 KORFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
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KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
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; Pred. No. 1.20
22; Mismatches
                                                                                                                                                                                                                                                                                                                                        Score 455.5; DB 1;
Pred. No. 2.8e-36;
21; Mismatches 42;
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b

- human

human papillomavirus type ME180 uman papillomavirus type ME180

ME180

(provirus)

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E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502
R;Volpers, C:; Streeck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: A38502
A;Status: translation not shown
A;Status: translation not shown
A;Residues: 1-188 <VOL>
A;Cross-references: UNIPROT:P24835; UNIPARC:UPI00001383D2; GB:M62849; EMBL:M38185; NID:C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger CCCC motif
F:102-68/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: host Homo sapiens (man)
C;Pate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5560, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical
A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: C40509
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <REU>
A;Cross-references: UNIPAROT:P27962; UNIPARC:UPI000000082F; GB:M73258
C;Superfamily; papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;132-68/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: host Homo sapiens (man)
Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KKORFHNIRGRWTGRCMSCCRSS-----RTRRETQL 151
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                                                                                                                                                                                                                                                                                                                   Similarity
                                           KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                 ACQSCIKFYAKIRELRYYSDSVYATTLENITNTKLYNLLIRCMCCLKPLCPAEKLRHLNS 123
                                                                                                                                       VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                    FQDPQERPRKLPQLCTBLQTTIHDIILBCVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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SKRRFHKIAGNFTGQCRHCWTSKREDRRTRQETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPBBKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
                                                                                                                                                                                             FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                          zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                55.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.4%; Score 451.5; DB 1; 55.1%; Pred. No. 6.8e-36;
                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                Score 449.5; DB 1;
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                              Mismatches
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158
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RESULT

RESULT 16 W6WL56 E6 protein .

human

papillomavirus

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E6 protein - human papillomavirus type 26 (;Species: human papillomavirus type 26 (;Species: human papillomavirus type 26 (;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 (;Accession: $36544 R.Pelius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 A.;Description: Primer-directed sequencing of human A.Reference number: $36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W6WLR1

86 protein - rhesus papillomavirus (type 1)

C;Species: rhesus papillomavirus
C;Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P36807; UNIPARC:UPI00001383C5; EMBL:X74472; NID:g396956; PID:C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P22159; UNIPARC:UP100001383EE; EMBL:M37717 C;Superfamily: papillomavirus E6 protein; C;Keywords: DNA binding; early protein; transforming protein; zinc finger C;Keywords: DNA binding; early protein; transforming protein; zinc finger E;60-96/Region: zinc finger CCCC motif
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A; Residues: 1-150 < DEL>
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Best Local :
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121
                                                                                             61
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                                                                                                                                                                                                                  1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                             AACKRCVIFYSKITEYRRYTCSVYGATLEALTKKSLCNLLIRCHRCQMPLGPEEKQRIVD 120
                                             KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                           MFEDPRERPRTLHELCESLNTTLQNLQVQCVYCKETLQWADVYNFAICDLRVVYRDRSPY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PICLRFYSKIRKYRRYEYSIYGCTLERRTRKQLVEVLIRCYCCQKPLCPIEKQRHVDQGQ
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EKRRFHEIAGOWKGLCTNCWR-PRRQTETQV
                                                                                                                                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                             52.6%; Score 436.5; DB 2; 55.0%; Pred. No. 1.7e-34;
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Pred. No. 1.6e-34;
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150
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$36503

E6 protein - human papillomavirus type 30

C;Species: human papillomavirus type 30

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: $36503

R;Delius, H.; Hofmann, B.

submitted to the EMBI Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-155 <LOE>
A;Cross-references: UNIPROT:P24836; UNIPARC:UPI00001383E0
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F. J. Gen. Virol. 70, 3099-3104, 1989
A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers. A;Reference number: A33377; MUID:90063558; PMID:2555440
A;Accession: A33377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-155 < DRL's
A; Cross-references: UNIPARC: UPI00001383E0; EMBL: X74483; NID: 9397053; PIDN: CAA52596.1;
A; Cross-references: UNIPARC: UPI00001383E0; EMBL: X74483; NID: 9397053; PIDN: CAA52596.1;
C; Superfamily: papillomavirus E6 protein;
C; Keywords: DNA binding; early protein; transforming protein; zinc finger
F; 33-69/Region: zinc finger CCCC motif
F; 106-142/Region: zinc finger CCCC motif
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C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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A; Residues: 1-153 < DEL>
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A; Accession: $36503
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A; Accession: S36579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: human
;Date: 31-Dec-19
                                                                                                                                                                                                                        Matches
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Best Local :
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Best Local
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31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                            Similarity
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KQRFHNIRGRWTGRCMSCCRSSRTRRET
                                                                                       VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLDK 121
                                                                                                                                                                      FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KORFHNIRGRWTGRCMSCCR-SSRTRRET 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                              VCNFCLLFYSKVRKIRHYNYSLYGASLVALTKKELFDLLIRCYRCQQPLTPEEKQLHCEY
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                                                                                                                                           FENTGERPRTVHHLCEVQETSLLELQLQCVYCKKELSSSEVYNFACKDLRLVYREDSPYA
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                        46.4%;
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56.4%; Pred. No. 1.6e-33;
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                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                                                          Score 385.5;
Pred. No. 1.3
                        149
                                                                                                                                                                                                                     1.3e-29;
ches 47;
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                                                                                                                                                                                                                                                           DB 2;
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RESULT 18
$36527
$6 protein - human papillomavirus type 53
$C;Species: human papillomavirus type 53
$C;Dace: 20-Feb-1995 #sequence_revision 20-Feb-C;Accession: $36527
$R;Delius, H.; Hofmann, B.
$submitted to the EMBL Data Library, August 19;
$commaccription: Primer-directed sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A,Residues: 1-155 <TAW>
A;Rosidues: 1-155 <TAW>
A;Cross-references: UNIPROT:Q80955; UNIPARC:UPI00001383E6
A;Cross-references: UNIPROT:Q80955; UNIPARC:UPI00001383E6
A;Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:7C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc
C;Keywords: DNA binding; early protein; transforming protein; zinc
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-154 <DEL>
A;Cross-references: UNIPROT:P36815; UNIPARC:UPI00001383DE;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type A;Reference number: A44890; MUID:92129556; PMID:1663515
A;Accession: A44890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 66
C;Species: human papillomavirus type 66
C;Date: 31-Mar.1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A44890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.R.; Beaudenon, S.; Favre, M.; Orth, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KKORFHNIRGRWTGRCMSCCR 141
                                                                                                                                   61 AVXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                              1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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HKRRFHYIAYAWTGSCLOCWRHT-SROATE 152
                                               KKORFHNIRGRWTGRCMSCCRSSRTRRETQ 150
                                                                                                    AVCRVCLLFYSKVRKYRYYKYSVYGATLESITKKQLSDLSIRCYRCQCPLTPEEKQLHCE 123
                                                                                                                                                                                                            I FSNTQERPRSLHHLSEVLQI PLLDLRLSCVYCKKELTSLELYRFACI ELKLVYRNNWPY
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#sequence_revision 20-Feb-1995
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                                                                                                                                                                                                                                                                                                                   44.9%; Score 372.5; DB 2; 50.7%; Pred. No. 2.2e-28; tive 20; Mismatches 53;
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Pred. No. 5.4e-29;
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A,Title: DNA sequence and genome organization of genital human A;Reference number: A90975; MUID:84131949; PMID:6321162
A;Accession: E20558
A;Molecule type: DNA
A;Residues: 1-150 <SCH>
A;Cross-references: UNIFROT:P06462; UNIPARC:UPI00000028A; GB:XC;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein - human papillomavirus type 6b C;Species: human papillomavirus type 6b C;Species: human papillomavirus type 6b C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004 C;Accession: E20558 R;Schwarz, E.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfsp EMBO J. 2, 2341-2348, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein - human papillomavirus type 43
C(species: human papillomavirus type 43
A,Note: host Homo sapiens (man)
A,Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
A;Titol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types
A;Reference number: A34144; MUID:89259065; PMID:2542593
A;Accession: A34144; MUID:89259065; PMID:2542593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P19709; UNIPARC:UPI00001383D6; GB:M27022; NID:g341596; C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
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Best Local
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                                                          132 WIGRCMSC 139
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                                                                                                   73
                                                                                                                                                                                    13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYFYAACACCLEFHG 72
                                                                                                                                                                                                                       12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
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                   WKGRCLHC
                                                                                                 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQFHGKISQYRHFDYAAYADTVEEETKQTVFDLCIRCCKCHKPLSPVEKVQHIVQKAQFF 127
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Pred. No. 5.4e-24;
77: Mismatches 55;
                                                                                                                                                                                                                                                                                      Score 304; DB 1;
Pred. No. 7.3e-22;
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                         DB 1; Length 150
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S15621
E6 protein
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W6WL44
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A; Residues: 1-150 <LOE>
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A; Residues: 1-153 <HIR>
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E6 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15621
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P22158; UNIPARC:UPI00001383E1; EMBL:X55965; N C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; transforming protein; zinc finger F;29-65/Region: zinc finger CCCC motif F;102-138/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types
A;Reference number: A34144; MUID:89259065; PMID:2542593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 44
c;Species: human papillomavirus type 44
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: B34144
C;Accession: B34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
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Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus
A;Reference number: S15614; MUID:91188699; PMID:1964523
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: DNA binding; early protein; transforming protein; F;31-67/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P19710; UNIPARC:UPI00001383D7; GB:M27023; NID:g341597; PIDN:
C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                     F;104-140/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AAAKURQYRHWHYSCYGDTVETETGIPIPQLFMRCYICHKPLCWEEKEALLVGNKRFHKI
                                                                                                                                                                                                                                            10 RKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKF
                                                                                                                                                                                                                                                                                                                 l Similarity 53; Conserv
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DTWKGRCFHCWTS
                                                                                                   QKVNQFRHFNYAGYAVTVBEETNKSILDVLIRCYLCHKPLCHVEKVRHILDKARFIKLQ
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                                                 GRWTGRCMSCCRS 142
                                                                                                                                                     YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                       QSIDQLCKECNIPMHNLQILCVFCRKTLSTAEVYSFAYKQLYVVYRGNFPFAACAICLEL
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Pred. No. 9.3e-22;
3; Mismatches 51
                                                                                                                                                                                                                                                                                                              Score 301; DB 1;
Pred. No. 1.4e-21;
8; Mismatches 52
                                                                                                                                                                                                                                                                                                                 52;
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A;Molecule type: DNA
A;Residues: 1-150 <DAP>
A;Residues: 1-150 <DAP>
A;Cross-references: UNIPROT:P04019; UNIPARC:UPI00001383B7; GB:M14119; NID:g333026; PIDN:
A;Cross-references: UNIPROT:P04019; UNIPARC:UPI00001383B7; GB:M14119; NID:g333026; PIDN:
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
C;Keywords: DNA binding; early protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein - human papillomavirus type 11
c;Species: human papillomavirus type 11
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A03684
R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6 protein - human papillomavirus type 2a C;Species: human papillomavirus type 2a A;Note: host Homo sapiens (man) C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004 C;Accession: S15614 R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 151, 124-130, 1986
A;Title: The nucleotide sequence and genome organization of human papilloma virus type A;Reference number: A94338; MUID:86181601; PMID:3008427
A;Accession: A03684
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A;Title: A comparative sequence analysis of two human papillomavirus (HPV)
A;Reference number: S15614; MUID:91188699; PMID:1964523
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A; Residues: 1-159 <HIR>
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Best Local Similarity
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                                              123 QRFHNIRGRWTGRCMSC 139
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                                                                                            CACCLELQGKINQYRHFNYAAYAPTVEEETNEDILKVLIRCYLCHKPLCEIEKLKHILGK 123
                                                                                                                                     XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKK 122
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                                                                                                                                                                                                                               QDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAV 62
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                                                                                                                                                                                   KDASTSATSIDQLCKTFNLSLHTLQIQCVFCRNALTTAEIYAYAYKNLKVVWRDNFPFAA 63
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                  35.4%; Score 294; DB 1; 35.8%; Pred. No. 6.6e-21;
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                                                                                                                                                                                                                                                                                 33;
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S36497
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S36584
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protein 28

human

papillomavirus

type 40

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C;Accession: S36584
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human
A;Reference number: S36469
A;Accession: S36594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6 protein - human papillomavirus type 7
C;Species: human papillomavirus type 7
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P36800; UNIPARC:UPI00001383B3; EMBL:X74463; NID:g397060; PID:C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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A; Residues: 1-159 < DEL >
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A; Residues: 1-154 < DEL>
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                                                                                                                                                                                                                                                                                     Query Match 35.0%; Score 290.5; DB 2; Length 154; Best Local Similarity 37.1%; Pred. No. 1.5e-20; Matches 53; Conservative 30; Mismatches 57; Indels 3
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Best Local 9
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mes 56; Conservative
130
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                                                                                                                                         70 YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                                                          10 RKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AAGKLRQYRHWHYSCYGDTVETETGIPIPQLFMRCYICHKPLSWEEKEALLVGNKRFHNI
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                                                                                                                                                                                            RTLFELCDQCNITLPTLQINCIFCNSILQTAEVLAFAFRELYVVWRNDFPFAACVKCLEF
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                                             GRWTGRCMSC---CRSSRTRRET 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGRWTGRCMSC 139
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DSWTGYCLHCWKKCMEKGQRSET 152
                                                                                              YGKVNQYRNFRYAAYAPTVEEETGLTILEVRIRCCKCHKPLSPVEKTNHIVKKTQFFKLQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.2%; Score 292; DB 2;
42.7%; Pred. No. 1.1e-20;
ative 21; Mismatches 54
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C;Species: human pap
C;Date: 20-Feb-1995
C;Accession: S36555
R;Delius, H., Hofman
$36509

86 protein - human papillomavirus type 32
C;Species: human papillomavirus type 32
C;Date: 20-Feb-1995 #sequence_revision 20-
C;Accession: $36509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar A;Reference number: A42955; MUID:92391075; PMID:1325697
A;Reference number: A36818
A;Molecule type: DNA
A;Residues: 1-150 <VAN>
A;Residues: 1-150 <VAN>
A;Cross-references: UNIPARC:UDI00001383ED; EMBL:X62844; NID:g61010; PIDN:CAA44655.1; PIIC C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein; transforming protein; zinc finger
C;Reywords: DNA binding; early protein; transforming protein; zinc finger
F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - pygmy chimpanzee papillomavirus (type 1)
C;Speciles: pygmy chimpanzee papillomavirus
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C;Accession: A36818
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.;
Virology 190, 587-596, 1992
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submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human
A;Reference number: $36469
A;Accession: $36555
A;Molecule type: DNA
A;Residues: 1-154 <DEL>
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C;Keywords: DNA binding; early protein; nucleus; zinc finger
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                        CEWKGRCFHCWTS
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                              20-Feb-1995 #text_change
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                                           09-Jul-2004
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C;Accession: A42955
R; van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G Virology 190, 587-596, 1992
A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar. A;Reference number: A42955; MUID:92391075; PMID:1325697
E6 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E39451
C;Philipp, W.; Honore, N.; Sapp, M.; Cole, S.T.; Streeck, R.E.
                                                                                                                                         RESULT
W6WL42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q02269; UNIPARC:UPI00001383B9; EMBL:X62843; NID:g60295; PIDN C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; transforming protein; zinc finger F;31-67/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 13
C;Species: human papillomavirus type 13
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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W6WL13
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C;Keywords: DNA binding; early protein; nucleus; zinc finger
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submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types
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A; Residues: 1-150 < VAN>
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A; Residues: 1-142 < DEL>
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wes 49; Conserv
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                                                                                                                                                                                                                                                                                 GRWTGRCMSCCRS 142
                                                                                                                                                                                                                                                                                                                                                                      YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
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                                                                                                                                                                                                                                   SSWKGRCFHCWSS
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40.9%; Pred. No. 7e-20;
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A;Reference number: A39451; MUID:92087479; l
A;Accession: E39451
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-150 < PUT-
A;Croc-
S36550

E6 protein - human papillomavirus type 3

C;Species: human papillomavirus type 3

C;Species: human papillomavirus type 3

C;Pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S36550

C;Accession: S36550

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469
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A;Accession: S36532
A;Accession: Sype: DNA
A;Residues: 1-148 <DEL>
A;Cross-references: UNIPROT:P36802; UNIPARC:UPI00001383B6; EMBL:X74465;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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E6 protein - human papillomavirus type 10
C;Species: human papillomavirus type 10
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36532
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
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Similarity 41.7%;
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Pred. No. 1.1e-15;
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Pred. No. 2e-18;
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A; Description: Primer-directed sequencing of human papillom A; Reference number: $36469 A; Accession: $36479 A; Molecule type: DNA A; Residues: 1-141 < DEL> A; Residues: 1-141 < DEL> A; Cross-references: UNIPROT: P36805; UNIPARC: UPI00001383BC; C; Superfamily: papillomavirus E6 protein C; Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E6 protein - human papillomavirus type 49
c;Species: human papillomavirus type 49
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36567
R;Delius, H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer_directed sequencing of human
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A;Residues: 1-152 <DEL>
A;Residues: 1-152 <DEL>
A;Cross-references: UNIPROT:P36799; UNIPARC:UPI00001383B0; EMBL:X74462;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                               E6 protein - human papillomavirus type C;Species: human papillomavirus type 17 C;Date: 20-Feb-1995 #sequence_revision C;Accession: $36479
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                                                                                                                                                                                  R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-138 < DEL>
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;Delius, H.; Hofmann,
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                                                                                                                                                                                                                                                                                                                                                                                                                     RVRNRWKGVCRHC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFYSKISEYRHYCYS-VYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGRWTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPVKVCELAHHLNIPIWEVLLPCNFCTGFLTYQELLEFDYKDFNLLWKDGFVFGCCAAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                           cary, August sequencing of
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; Pred. No. 6.7e-15;
23; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 154; DB 2;
Pred. No. 1.3e-07;
0; Mismatches 65
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                                                                                                                                                                t 1993
of human
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                                                   EMBL: X74469; NID: g396932;
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E6 protein - human papillomavirus type la C;Species: human papillomavirus type la C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text C;Date: 0.; Katinka, M.; Yaniv, M. RyBo J. 1, 231-236, 1982
A;Reference number: A90970; MUID:84182467; PMID:6325156
A;Accession: B17475
                                                                                                                                                                                                                                                                                                     RESULT 38
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A;Recession: A43550
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-156 <HIR>
A;Residues: 1-156 <HIR>
A;Cross-references: UNIPROT:P27555; UNIPARC:UPI00001383D4; EMBL:X56147; NID:g60942; C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
E;42-78/Region: zinc finger CCCC motif
                  A;Molecule type: DNA
A;Residues: 1-140 <DAN>
A;Residues: 1-140 <DNIPACT:P06929; UNIPARC:UPI00001383BE; GB:V01116;
A;Cross-references: UNIPROT:P06929; UNIPARC:UPI00001383BE; GB:V01116;
R;Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W6WL41

E6 protein - human papillomavirus type 41
C;Specles: human papillomavirus type 41
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993
C;Accession: A43550
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Virus Res. 18, 179-190, 1990
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Comparative analysis of the human type la and bovine type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
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26.3%; Pred. No. 6.2e-06;
tive 23; Mismatches 75;
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Pred. No. 1.4e-06;
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A;Molecule type: DNA
A,Residues: 1-161 <DEL*
A,Residues: UNIGROT:P28833; UNIDARC:UPI00001383C4; EMBL:X74471; NID:g396948;
A;Cross-references: UNIGROT:P28833; UNIDARC:UPI00001383C4; EMBL:X74471; NID:g396948;
C;Superfamily: papillomavirus E6 protein; nucleus; zinc finger
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                 R;Delius, H.; Hofmann, B.
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the EMBL Data Library, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:P11302; UNIPARC:UP1000017495C; C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;17-55/Region: zinc finger CCCC motif F;90-129/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E6 protein - bovine papillomavirus type 2
c;Species: bovine papillomavirus type 2
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: H31169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A92993; MUID:83189357; PMID:6302319
A;Contents: annotation
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
                                                                                                                                                                                                                A; Description: Primer-directed A; Reference number: S36469 A; Accession: S36491
                                                                                                                                                                                                                                                                                                                                                            E6 protein - human papillomavirus type 25
C;Species: human papillomavirus type 25
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-139 < GRO>
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A; Accession: H31169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Matches 37; Conserv
Query Match
Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 LEQQ -- YNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR-WTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LACVWCREPLIEVDAFRCMIKDFHVVYRDGVKFGACTTCLE--NCLDKERRLWKGVPVTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLLEFVLYYQESYEVPEIEEILDRPLLQIELRCVTCIKKLSVAEKLEVVSNGERVHRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEBKQRHLDKKQRPHNIR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTVRQLSESICIPYIDVLLPCNFCNYFLSNAEKLLFDHFDLHLVWRDNLVFGCCQGCART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBAQLLHGKSLDRLCIRCCYCGGKLTKNEKORHVLYNEPFCKTRSNIIRGRCYDCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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28.0%; Pred. No.
--ive 21; Mismatches
  15.9%; Score 132; DB 2;
25.2%; Pred. No. 1.9e-05;
ative 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
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Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 134.5; DB 1; Pred. No. 9.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                   papillomavirus
                                             Length 161
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RESULT 42
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S28510
E6 protein -
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                                                                                            R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of hu
                                                                                                                                                     E6 protein - human papillomavirus type 15 C;Species: human papillomavirus type 15 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: $36473
                                                         A; Reference number: $36469
A; Accession: $36473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;van Ranst, M.; Tachezy, R.; Pruss, J.; Burk, R.J. Nucleic Acids Res. 20, 2889, 1992
A;Title: Primary structure of the E6 protein of Micromys A;Reference number: S22955; MUID:92310995; PMID:1319576
  A;Cross-references:
                  A; Molecule type: DNA
A; Residues: 1-141 <DEL>
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A; Residues: 77-204 < VAN2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P30735; UNIPARC:UP100001383EA; EMBL:X65201; NID:g60575; A;Note: the source is designated as Mastomys natalensis papillomavirus R;van Ranst, M.; Tachezy, R.; Pruss, J.; Burk, R.D.
Nucleic Acids Res. 20, 2889, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: S28509
A;Accession: S28510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S28510; S22956
R;van Ranst, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 protein - multimammate rat papillomavirus (fragment);Species: multimammate rat papillomavirus
;Species: multimammate rat papillomavirus
;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
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Best Local
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                                                                                                                                                                                                                                                                                                                                        KQRHLDKKQRFHNIRGRWTGRCMSC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLL------IRCINXQKPLCPEE 114
                                                                                                                                                                                                                                                                                                                    KLECAERGESFAKVRGQWRARCRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGSWKGICRLC 154
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UNIPROT: P36804; UNIPARC: UPI00001383BB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129.5; DB 2;
Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -plicecvyckQQLLRREVYDFAFRDLCIVYRDGNPYAVXDK 65
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                                                                                                                                                                                                                                                                                                                    204
                                                                                                human
                                                                                              papillomavirus types
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EMBL: X74468;
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NID:g396924;
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E6 protein - human papillomavirus type 18
C7.Species: human papillomavirus type 18
C7.Species: human papillomavirus type 18
C7.Accession: I56705
R7.Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.;
R7.Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.;
J. Virol. 62, 1640-1646, 1988
A;Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcr
A;Reference number: I56705; MUID:88188247; PMID:2833614
A;Recession: I56705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:Q90133; UNIPARC:UPI00000EDD5F; GB:M20324; NID:g1839
C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              E6 protein - cottontail rabbit papillomavirus
C;Species: cottontail rabbit papillomavirus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
C;Accession: A03686
                                                                                                                                                                                                                                                                                                                                         R;Giri, I.; Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope)
A;Reference number: A94027; MUID:85166175; PMID:2984661
A;Accession: A03686
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IS6705
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                                                                                                                                                                                                                                     C; Keywords:
                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI0000000953 C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-273 <GIR>
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                                                                                                                                                                    Best
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les 36; Conserv
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                                                                                                                                                                                                                                   DNA binding; early protein; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRC-INXQKPLCPEE---KQRH-----L 119 : | | : : | |: : |: : 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFATAQFEFSNFYEQSVCSWEIEIVEQKPVGDIIIRCKFCLKKLDLIEKLDICYKEEQFH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPFSVQQLADTLCIPLVDILLPCRFCQRFLTYIELVSLNRKGLQLIWTEEDFVFACCSSC
                                                                PRSLEKLQQILQISLEDLPFGCIFCGKLLGAAEKQLFKCTGLCIVWHKGWPYGTCRDCTV 65
                                                                                                      PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.5%;
                                                                                                                                                                    15.3%;
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                                                                                                                                                     21;
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                                                                                                                                                Score 127; DB 1;
Pred. No. 9.5e-05;
1; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 128.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 127; DB 2; I
Pred. No. 2.1e-05;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 57;
                                                                                                                                                                                           Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                        papillomavirus.
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S36485

E6 protesin - human papillomavirus type 19
C;Species: human papillomavirus type 19
C;Pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #tc
C;Accession: S36485
R;Pelius, H: HOfmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papar, A;Accession: S36489
A;Accession: S36489
A;Molecule type: DNA
A;Residues: 1-166 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 45
S36538
E6 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein - human papillomavirus type 12 (;Speciles: human papillomavirus type 12 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S36538 R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-157 <DEL>
A;Residues: 1-157 <DEL>
A;Cross-references: UNIPROT:P36803; UNIPARC:UPI00001383B8; EMBL:X74466; NID:g396910;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human
A;Reference number: S36469
A;Accession: S36538
                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P36806; UNIPARC:UPI00001383BD; EMBL:X74470 C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; nucleus; zinc finger
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Best Local :
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 149
                                  129
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                                                                      89
                                                                                                        69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKKORFHNIRGRWTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSCALDLYCHLALTAPALEAEALVGQEISSWFMRCTVCGRRLTIPEKIELRARNCTLCCI 125
 RDSWKGICRLC 159
                                    RGRWTGRCMSC 139
                                                                      ATATFEFNEFYEHTVTGREIEFVTGKSVFDIDVRCQNCMRYLDSIEKLDICGRRLPFHKV 148
                                                                                                        FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI 128
                                                                                                                                            PATIAGLAALLEIPLDDCLVPCNFCGKFLSHLEACEFDDKRLSLIWKGHLVYACCRWCCT 88
                                                                                                                                                                              PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELPTTIKELADLLDIPLVDCLVPCNFCGKFLDFLEVCDFDKKQLTLIWKGHFVTACCRSC
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                                                                                                                                                                                                                                    14.8%;
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                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                  Score 123; DB 2;
Pred. No. 0.00014
24; Mismatches 7
                                                                                                                                                                                                                                                     DB 2; Length 166
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A; Residues: 1-137 < CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: C18151
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                            Query Match
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 HNIRGRWTGRCMSC 139
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LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR-WTGRCMSCCR-SSRT 145
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                                                                                                          Conservative
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24.6%; Pred. No. 0.00
ative 31; Mismatches
                                                                                                                           14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                        . 16;
                                                                                                            Mismatches
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A;Cross-references: UNIPROT:P06931; UNIPARC:UPI0000033CF0; GB:X02346; GB:J02044; GB:N
R;Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A;Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus garactive analysis of the human type 1a and bovine type 1 papillomavirus garactive annotation
R;Androphy, E.J.; Schiller, J.T.; Lowy, D.R.
Schience 230, 442-445, 1985
A;Title: Identification of the protein encoded by the E6 transforming gene of bovine
A;Reference number: A94282; MUID:86018841; PMID:2996134
A;Contents: annotation; identification of the protein
C;Comment: This protein is present in the cell nucleus and the cellular membrane.
C;Superfamily: papillomavirus E6 protein; transforming protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein - bovine papillomavirus type 1
(;Species: bovine papillomavirus type 1
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C18151
R;Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
A;Title: The primary structure and genetic organization of the bovine papil.
A;Reference number: A93289; MUID:83012974; PMID:6289124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P36801; UNIPARC:UPI00001383B5; EMBL:X74464; NID:g397068; C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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C;Species: human papillomavirus type 9
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36590
                                                            28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGN-PYAVXDKC
LDCLWCREPLTEVDAFRCMVKDFHVVIREGCRYGACTICLENCLATERRLWQGVPVTGEE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AYASAQLEFTHFFQFAVVGKDIETVEGTAIGNICIRCRYCFKLLDLVEKLATCYKFEQF
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                                                                                                                                                                   Score 119; DB 1;
Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00018;
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                                                                                                                                                                                               Length 137
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A;Reference number: A93019; MUID:86200410; PMID:3009874
A;Accession: A03685
A;Molecule type: DNA
A;Residues: 1-155 <FUC>
A;Cross-references: UNIPROT:P06428; UNIPARC:UPI00001383B4; GB:M12737; NID:g333074
A;Cross-references: UNIPROT:P06428; UNIPARC:UPI00001383B4; GB:M12737; NID:g333074
A;Note: this ORF is not annotated in GenBank entry PPH8CG
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;319-75/Region: zinc finger CCCC motif
F;3112-148/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;ACCEBBION: A03001
R;Fuche, P.G.; Iftner, T.; Weninger, J.; Pfister, H.
J. Virol. 58, 626-634, 1986
A;Title: Epidermodysplasia verruciformis-associated human papillomavirus 8: genomic sequal control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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86 protein - human papillomavirus type 8

C;Species: human papillomavirus type 8

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
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A;Title: Genome organization and taxonomic A;Reference number: A35324; MUID:90281611; A;Accession: A35324
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C;Keywords: DNA binding; early protein; transforming
F;40-76/Region: zinc finger CCCC motif
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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A; Residues: 1-156 < KIY>
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Best Local S
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                                                                                                                                      Matches
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ELPSTIKELAAALGIPLODCSVPCNFCGNFLDFLELCEFDKKRLCLIWKN---YVVTACC
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                                                                                                                                      Conservative
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                                                                                                                                  27;
                                                                                                                                                                   Score 118; DB 1;
Pred. No. 0.0004;
                                                                                                                                      Mismatches
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PMID:2162112
                                                                                                                                                                                                       DB 1;
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E6 protein - human papillomavirus type 5b
C;Species: human papillomavirus type 5b
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: B40480
R;Yabe, Y; Sakai, A; Hitsumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A;Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplific A;Reference number: A40480; MUID:91306467; PMID:1649510
A;Accession: B40480
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W6WLB5
E6 protein -
                                                                                                                                                                         A;Cross-references: UNIPARC:UPI000017495B
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
E;41-77/Region: zinc finger CCCC motif
E;114-150/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                                             R;Zachow, K.R.; Ostrow, R.S.; Faras, A.J.
Virology 158, 251-254, 1987
A;Title: Nucleotide sequence and genome organization of human papillomavirus type
A;Reference number: A94360; MUID:87207670; PMID:3033892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein - human papillomavirus type 5
C;Species: human papillomavirus type 5
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Feb-1997
C;Accession: F26277
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A; Residues: 1-157 <ZAC>
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Best Local
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l Similarity 24.1%;
33; Conservative 2:
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Similarity
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ilarity 24.8%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                22;
                                                                           Score 113; DB 1;
Pred. No. 0.0012;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 116; DB L; L
Pred. No. 0.00063;
                                                                                82;
                                                                                                                             Length 157
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                                                                                Indels
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A;Molecule type: DNA
A;Residues: 1-135 <GRO>
A;Crose-references: UNIPROT:P03128; UNIPARC:UPI00001383EB;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
                                                                                                                                               E6 protein - deer papillomavirus
C;Species: deer papillomavirus
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Date: 78-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03687
R;Groff, D.E.; Lancaster, W.D.
J. Virol. 56, 85-91, 1985
A;Title: Molecular cloning and nucleotide sequence of deer papillomavirus.
A;Reference number: A93013; MUID:85293253; PMID:2993669
A;Accession: A03687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI0000178417; EMBL:X65200 A;NOte: the source is designated as Micromys minutus papillomavirus C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;38-74/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid se
A;Molecule type: DNA
A;Residues: 20-147 <VAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein - Old World harvest mouse papillomavirus (fragment) C;Species: Old World harvest mouse papillomavirus C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004 C;Accession: S28509; S22955 R;van Ranst, M.A. submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 20, 2889, 1992
A;Title: Primary structure of the E6 protein of Micromys
A;Reference number: S22955; MUID:92310995; PMID:1319576
A;Accession: S22955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P30734; UNIPARC:UPI0000170F1E; EMBL:X65200; NID:g60571; A;NOte: the source is designated as Micromys minutus papillomavirus R;van Ranst, M.; Tachezy, R.; Pruss, J.; Burk, R.D. Nucleic Acids Res. 20, 2889, 1992
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A; Accession: S28509
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A; Residues: 1-154 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           문
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRFHNIRGRWTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KD----CCFKGACIKCRRKLAFAEROKYQVCVGEADLVEAMVGSHVINLTVRCSECLALLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PO-ERPRKLPQLCTE------LQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRVCCGATATYEFNQFYEQTVLGRDIELASGLSIFDIDIRCQTCLAFLDIIEKLDCCGRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFHYKRLSLIWKDYCVFAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQPTRPYSFMELCREYTLEQLLKFLNVTLDTLMLPCHFCSSFMDLNNKASYLASQLKVIV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             minutus papillomavirus
                                                                GB:M11910; NID:g333021;
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                                                                   PIDN:
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        E6-I protein - human papillomavirus type 33 (fragment) (;Specise: human papillomavirus type 33 (fragment) (;Specise: human papillomavirus type 33 (fragment) (;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004 (;Accession: S23825; S23829 R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphors
                                                                                                                                                                                RESULT
                                                                                                                                                        S23825
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57

H.F.J.; Raaphorst,

P.M.C.;

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A;Molecule type: mRNA
A;Residues: 1-35 <SNI2
A;Cross-references: UNIPROT:Q81887; UNIPARC:UPI00000EBD75; EMBL:X64087; NID:g60286;
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S19909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-32 <SNI-2
A;Cross-references: UNIPROT:Q81885; UNIPARC:UPI00000F932A; EMBL:X64086; NID:g60282;
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S19906
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F
submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates
A;Reference number: S19906
A;Accession: S19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
S19906
                                                                                                                                                                                                                                                                          R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7
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A;Accession: S19909
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                                                                     Best Loc
Matches
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;Species: human papillomavirus type 33
;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                  ;Accession: S19909
                                                                                                                                                                                                                                                                                                                                                                     6-III protein - human papillomavirus type 33 (fragment);Species: human papillomavirus type 33
                                                                                                                                                                                                                                                                                                                                                  Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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Best Local
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                                                                                                          Query Match
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                                                                     Local Similarity 59.
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               LCTELQTTIHDIILECVYCKQQLLRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCTELQTTIHDIILECVYCKQQLLRRE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTLEQ--QYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYCVFCYCVLGKVEARRCYDKKIR---TVVRGGLRCAVCTACLEKGLYLERVLNAPQPVY 65
LCQALETTIHNIELQCVECKKPLQRSE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCQALETTIHNIELQCVECKKPLQRSE
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                                                                                       10.0%;
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                                                                       4.
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                                                                                     Score 83; DB 2
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83; DB 2
Pred. No. 0.19;
                                                                     Mismatches
                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
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                                                                       7;
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                                                                                                          Length 35;
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                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its putative E7
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                                                                       Gaps
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                                                                                                                                                                                                                                                                                mRNA via
                                                                                                                                                                                     PIDN
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E6 protein - European elk papillomavirus C;Species: European elk papillomavirus C;Species: European elk papillomavirus C;Chate: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004 C;Accession: A29499; F94457; F94506 C;Accession: A29499; F94457; F94506 R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U. Gene 50, 195-205, 1986 R,Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U. Gene 50, 195-205, 1986 R,Title: Organization and expression of the transforming region from the Europe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 58
T02749
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A;Description: HPV type 33 in a tonsillar carcinoma
A;Reference number: S19906
A;Accession: S23825
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R;Grafi, G.; Burnett, R.J.; Helentjaris, T.; Larkins, B.A.; deCaprio, J.A.; Sellers, W. submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G1/S transition control protein RB - maize (fragment) N;Alternate names: retinoblastoma-related protein
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  A;Cross-references:
                    A; Molecule type: DNA
A; Residues: 1-135 < AHO>
                                                            A; Reference number: A91567; A; Accession: A29499
                                                                                                                                                                                                                                              M6WLEP
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A;Experimental source: strain W64A+; endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: A maize cDNA
A;Reference number: Z14715
A;Accession: T02749
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A; Residues: 1-47 < SNI>
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                                                                                                                                                                                                                                                                                                                                                             ---YNKPLCDLLIRCINXQKPLCPEE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                             RDGNPYAVXDKCLK-----FYSKISEY-----RHYC-----YSVYGTTLEQQ-
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                                                                                                                                                                                                                                                                                                                          TLFFNRHIDQLILCCLYGVAKVCQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 79.5; DB 2; Length 471; ilarity 23.3%; Pred. No. 5.4; Conservative 23; Mismatches 48; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                       NPVGGNEKCADVTIHIFFSKILKFPAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 300
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  UNIPROT: P11331; UNIPARC: UPI00001383EC; GB: M15953;
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                                                                               expression of the transforming 7; MUID:87219878; PMID:3034730
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NID:g333025;
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zyxin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence
C:Accession: G02845
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                                                                                                                                                                                                                                                                                                           A;Gene: zyx
C;Keywords: duplication
F;384-436/Domain: LIM metal-binding
F;444-495/Domain: LIM metal-binding
F;504-565/Domain: LIM metal-binding
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G02845
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A;Molecule type: mRNA
A;Residues: 1-572 <BEC's
A;Cross-references: UNIPROT:Q15942; UNIPARC:UPI00000424F2; EMBL:X94991; NID:g1155087
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R;Beckerle, M.C.
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A; Molecule type: DN
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                                                                                                                                                                                                         1 MFQD---PQERPRKLPQLC------TELQTTIHDIILECVYCKQQLLRREVY 43
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MSC 139
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                                                                                                    SLEGAPYCEGCYTDTLEKCNTCGEP--ITDRMLRATGK--AYHPHCFTCVVCARPLEGTS
                               FIVDQANRPHCVPDYHKQYAPRCSVCSEPIMPEPGRDETVRVVALDKNFHM-
                                                              -LEQQYNKPLC-----DLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC 136
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                                                                                                                                                                                                                                                            Score 77.5;
Pred. No. 10
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repeat
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CiSpecies: Homo mapiens (man)
C;Date: 16-Uul-1999 #sequence-
C;Date: 16-Uul-1999 #sequence-
C;Accession: T09483
R;Smedley, D.P.; Hamoudi, R.; Clark, J.; Warren, W.; Abdul-Rauf, M.; Somers, mubmitted to the EMBL Data Library, November 1997
A;Description: RAMP, a novel gene encoding a Cys-rich protein.
A;Reference number: Z16688
A;Accession: T09483
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T09483
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C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11515
R;Woychik, R.D.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A;Title: 'Formins': proteins deduced from the alternative transcripts of the limb A;Reference number: S11515; MUID:90363291; PMID:2392150
A;Accession: S11515.
  RESULT
S44810
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A;Molecule type: mRNA
A;Residues: 1-699 <SME>
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C;Genetics:
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;Residues: 1-1468 <WOY>
;Cross-references: UNIPROT:Q05860; UNIPARC:UPI000027927; EMBL:X53599; NID:g52877; PIDN
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Gene: RAMP
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                                                                                                                                                                                                                                         362
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                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 --HNCYQVREGPDITSLSQQPNEHPGDIFFKQTPTKNILTELYKLTAEKERLLDSLLRSD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                            25 DIILECVYCKQQLLRR-----EVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
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                                                                              ATKELDGVVRDFCSEDCCKKFQD----
                                                                                                                     KQRHLDKK----
                                                                                                                                                        VTYCEYCQEEKTLHETVNFSGVKRPFCSEGCKLLYKQDFARRLGLRCVTCNYCSQLCKKG 465
                                                                                                                                                                                                RHYC-YSVYGTTLEQQYN-----KPLCD------LLIRCI--NXQKPLCPEE 114
                                                                                                                                                                                                                                       DIQLKCNYCKNSFCSKPEILEWENKVHQFCSK-----TCSDDYKKLHCI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NILG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRHYCYSVYG----TTLEQQYNKPLCDLLIRCINXQKPL-----CPEEKQRHLDKKQRFH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTELOTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CT-LQ--LHNPIABLCYISFYLPKGEVRGFSYKGTVTLDRSNNAF------
                                                                                                                                                                                                                                                                                                                                                                                                13q11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 77.5; llarity 27.4%; Pred. No. 25; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537
                                                                                                                                                                                                                                                                                                                                    9.3%; Score 77; DB 22.2%; Pred. No. 14;
                                                                                                                   -----QRFHNIRGRW---TGRCMSCCRSSRTRRE 148
                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                              -WYYKAARC-DCCKSQGTLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                      Length 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1468;
                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                                                                                                                                                                                                 Gaps
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                RESULT
T21125
hypothetical protein F19H8.2 -
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F44B9.7 protein - Caenorhabditis elegans
G;Species: Caenorhabditis elegans
G;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44B10
R;Antonacci_Fulton, L.
R;Antonacci_Fulton, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 09-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71522; I38074
C;Accession: S71522; I38074
R;Hofferbert, S.; Burfeind, P.; Hoyer-Fender, S.; Lange, R.; Haidl, G.; Engel, Hum. Mol. Genet. 2, 2167-2170, 1993
A;Title: A homozygous deletion of 27 basepairs in the coding region of the hum.
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S71522
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, September 1993 A;Description: Sequence of the C. elegans cosmid F
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                                                                                                                                                                                                                                                                 A; Description: provides the sperm tail with stabilizing and zinc binding properties A; Note: one of the main component of the sperm tail
                                                                                                                                                                                                                                                                                                                                  A; Map position:
A; Introns: 107/2
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT:Q14990; A; Note: the nucleotide sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 138074; MUID: 94154698; PMID: 8111388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000017B6C2; EMBL:L23648; NID:g388585; PID:g388589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S44807
                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ODF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-250 < HOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outer dense fiber protein 2 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-400 < ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                  Query Match
Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                          95 PLCDLLIRCINXQKPLCPEEKQRHL------DKKQRFHNIRGRWTGRCM--SCCRSS 143
                                                                                        26 RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL------CYS------KRSRSC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPOSHIRESPOKETNLEKYSTGELCLYGRELVNDLNVKTSYLSTILKKVMERKPLN----
GLCDLYPCCLCDYKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMDEEROKRRAELEORFAIVISKTPPVEGHIWYQGKW 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLCPEEKQRHLDKKQRFHNI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QGENPNDLADQCKNALQRMSDIRQIIEKRREPTWKRMTGEDYIELMLDDSELKK 305
                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                             Conservative
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                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                  Score 75.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 2; Length 400; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                           UNIPARC: UPI0000130BD2; EMBL: X74614; submitted to the EMBL Data Library,
                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RGRW 132
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                                                                                                                                                                             36;
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                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                             Indels
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                                                                                                                                                                             37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the human
                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g474425;
August 1993
  124
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PID

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65

Caenorhabditis elegans

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C;Species: Go
C;Date: 31-De
C;Accession:
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S56100
             alpha-fetoprotein precursor - gorilla
C;Species: Gorilla gorilla (gorilla)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer dense fiber protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Steward, C.
submitted to the EMBL Data Library,
A;Reference number: Z19379
A;Accession: T21125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T21125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kim, Y.; Adham, I.M.; Haack, T.; Kremling, H.; Engel, W. Biol. Chem. Hoppe-Seyler 376, 431-435, 1995
A;Title: Molecular cloning and characterization of the bovine A;Reference number: S56100; MUID:96066278; PMID:7576240
                                                                                            RESULT 67
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A; Residues: 1-262 < KIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT:045378; A; Experimental source: clone F19H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-303 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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Gene: CESP:F19H8.2
                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q29077; UNIPARC:UPI0000130BD3; GB:X69513; NID:g1165146; PID;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                         PLCDLLIRCINXQKPLCPEEKQRHL-----DKKQRFHNIRGRWTGRCM--SCCRSS 143
                                                                                                                                                                                                                               RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWTGRCMS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RKYNLPEIEVNNSTLTSNSTHVQVSPLEQCLNFQK-ICAAKYKKHFACRQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QERPRKLPQLCTELQ-----FA 46
                                                                                                                                                      GLCDLYPCCLCDVKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLEQQYNKFLCDL-------LIRCINXQKPLCPEEKQRHLDKKQRFHNIRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRDLC----IVYRDG-----NPYAVXDKCLKFYSKISE-----YRHYCYSVYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESQGRLCPSWCGHLKSNETIVNILGAVGNSTTDLQDVSFECDDLKKNCLAVKKYNGHCYF 129
                                                                                                                                                                                                                                                                REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YRKKCLS
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                                                                                                                                                                                                                                                                                                      14; Mismatches
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                                        Score 74.5; DB 2; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  March 1997
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A,Molecule type: DNA
A,Residues: 1-609 <GIBs
A,Cross-references: UNIPROT:P02771; UNIPARC:UPI00000012A9; GB:M16110; NID:g773678; PIDN:I
A,Cross-references: UNIPROT:P02771; UNIPARC:UPI00000012A9; GB:M16110; NID:g773678; PIDN:I
R;MCVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumlauf
Hum. Mol. Genet. 2, 379-384, 1993
A,Title: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gen
A,Reference number: S37655; MUID:93278385; PMID:7684942
A,Accession: S37655
A,Accession: S37655
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A; Map Dosition: 4q11-12
A; Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 43
C; Superfamily: serum albumin; serum albumin repeat homology
C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-609/Product: alpha-fetoprotein #status predicted <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;29-202/Domain: serum albumin repeat homology <SA1>
                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000016A4DF; EMBL:Z19532; NID:g28527; PIDN:CAA79592.1; A;Note: the authors translated the codon TAT for residue 26 as Thr A;Mortnaga, T.; Sakai, M.; Wegmann, T.67; Tamaoki, T. Tamaoki, T. Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983
A;Title: Primary structures of human alpha-fetoprotein and its mRNA.
A;Reference number: A93961; MUID:83273664; PMID:6192439
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A;Title: Structure of the gorilla alpha-fetoprotein gene and the divergence A;Reference number: A37970; MUID:91169517; PMID:1706310
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A;Molecule type: mRNA
A;Residues: 1-609 <MOR>
A;Cross_references: UNIPARC:UPI0000012A9; GB:J00077; NID:g311348; PIDN:CAA24758.1;
                                                                                                                                                                   A; Accession: A93961
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A; Residues: 1-28 < MCV>
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;413-592/Domain: serum albumin repeat homology <SA3>
;2413-592/Domain: serum albumin repeat homology <SA3>
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;29-114,113-124,148-193,192-201,224-270,269-277,289-303,302-313,384-393,416-462,461-472,
;249/Binding site: bilirubin (Lys) #status predicted
;249/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Dugaiczyk,

PID:

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A;Mclecule type: protein
A;Mclecule type: protein
A;Residues: 'S',20-24,'O',26-30,'A',32-35,'E',37-39 <RUO>
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A;Cross-references: UNIPARC:UPI000017442C
R;Sakai, M; Morinaga, T; Urano, Y; Watanabe, K; Wegmann, T.G.; Ta
J. Biol. Chem. 260, 5055-5060, 1985
A;Title: The human alpha-fetoprotein gene. Sequence organization and
A;Reference number: A92520; MUID:85182629; PMID:2580830
A;Contents: annotation; gene, exons and introns
R;Aoyagi, Y; Ikenaka, T; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
A;Reference number: A90758; MUID:79001617; PMID:80265
A;Contents: annotation; metal binding
R;Aoyagi, Y; Ikenaka, T; Ichida, F.
Cancer Res. 39, 3571-3574, 1979
Cancer Res. 39, 3571-3574, 1979
                                                                                                                                                                                                                                                                                     Cancer Res. 39, 3571-3574, 1979
A;Title: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding abilantile: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding A;Reference number: A90759; MUID:80001710; PMID:89900
A;Contents: annotation; bilirubin binding
C;Comment: arrotation; bilirubin binding
C;Comment: AFP is synthesized by the fetal liver and yolk sac. It occurs in the plasma of trace amounts after birth. The serum level in adults is usually less than 40 ng/ml. A otrace amounts after birth. The serum level in adults is usually less than 40 ng/ml. A otrace amounts after birth. The serum level in adults is usually less than 40 ng/ml. A
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A;Cross-references: UNIPARC:UPI0000174421; GB:J00076
R;Cross-references: UNIPARC:UPI0000174421; GB:J00076
R;Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.;
Biochemistry 30, 5061-5066, 1991
Biochemistry 30, 5061-5066, 1991
A;Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.
A;Reference number: A23699; MUID:91242409; PMID:1709810
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A; Residues: 'S', 20-30, 'A', 32-37, 'A' <AOY>
A; Residues: 'S', 20-30, 'A', 32-37, 'A' <AOY>
A; Crose - references: UNIPARC: UPI000017442B
A; Ruoslahti, E.; Pihko, H.; Vaheri, A.; Seppala, M.; Virolainen, Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
A; Title: 20. Alpha fetoprotein: structure and expression in man A; Reference number: A93042; MUID:75018719; PMID:4138095
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A;Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>
A;Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>
A;Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174425
A;Yachnin, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.B.
R;Yachnin, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.B.
Biochim. Biophys. Acta 493, 418-428, 1977
A;Title: Studies on human alpha-fetoprotein. Isolation and characterization of monomeric
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Cancer Res. 37, 3663-3667, 1977
A;Title: Comparative Chemical structure of human alpha-fetoproteins
A;Reference number: A90757; MUID:78001760; PMID:71198
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Cancer Res. 37
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A;Residues: 'S',20-22,'S',24-35 <YAC>
A;Cross-references: UNIPARC:UPI000017442A
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A;Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
A;Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
A;Crose-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174423; UNIPARC:UPI0000174424
R;Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
J. Nucl. Med. Allied Sci. 34, 213-216, 1990
A;Tille: Characterization of in vitro expressed human alpha-fetoprotein as highly reproda;Reference number: A61480; MUID:91225826; PMID:1709209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 20, 415-422, 1982
A;Title: Structure and evolution of human alpha-fetoprotein deduced from partial
A;Reference number: A91497; MUID:83158778; PMID:6187626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: dimeric and trimeric forms have R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.
A:Map position: 4q11-4q13
A:Introns: 29/1; 46/2; 90/3; 1
C:Superfamily: serum albumin;
                                                                                                                                 A;Gene: GDB:AFP
A;Cross-references: GDB:119660; OMIM:104150
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    90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3;
lbumin; serum albumin repeat homology
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R.Mishio, H.; Gibbs, P.E.M.; minguerra, R.Mishio, H.; Gibbs, P.E.M.; minguerra, Gene 162, 213-220, 1995

Gene 162, 213-220, 1995

A;Title: The chimpanzee alpha-fetoprotein-encoding gene shows

A;Title: The chimpanzee alpha-fetoprotein-encoding gene shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: afp
A;Map position: 3p
A;Map position: 3p
A;Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3
C;Superfamily: serum albumin; serum albumin repeat home
C;Keywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
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JC4258
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F;413-592/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;22/Binding site: copper (Hi3)
F;229-114,113-124,148-193,192-201,224-270,269-277,289-303,302-313,384-393,416-462,461-472
F;299-114,113-124,148-193,192-201,224-270,269-277,289-303,302-313,384-393,416-462,461-472
F;249/Binding site: bilirubin (Lys) #status predicted
F;251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-609 <NIS>
A;Cross-references: UNIPROT:Q28789;
C;Comment: This protein is a plasma
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                                                                                                                                                                                                                                                                                                                                                           ;221-394/Domain: serum albumin repeat homology <SA2>
;413-592/Domain: serum albumin repeat homology <SA3>
;42,251/Binding site: carbohydrate (Asn) (covalent) #status
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Best Local
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                                          INXQKPL-C---PEEKQRHLDKKQ 123
                                                                                                                                                                                                                    QERPRKIPQICTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INXQKPL-C---PEEKQRHLDKKQ 123
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FQTENPLECQDKGEEELQKYIQESQ
                                                                                                                                 ------RPGNPYAVXDKCLKFYSKISEY--RHYCYSVYGTTLEQQYNKPLCDLLIRC 103
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                                                                                                                                                                                                                                                                                           Score 74.5;
Pred. No. 21
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Pred. No. 21;
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C;Accession: F96784

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Lit, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, R.; C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: F96784
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R;Popovici, C.; Adelaide, J.; Ollendorff, V.; Chaffanet, M.; Guasch, G.; Jacrot, M.; Ler Proc. Natl. Acad. Sci. U.S.A. 95, 5712-5717, 1998
A;Title: Fibroblast growth factor receptor 1 is fused to FIM in stem-cell myeloprolifera A;Reference number: Z22919; MUID:98245146; PMID:9576949
A;Accession: T45119
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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A; Residues: 1-524 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9UBW7; UNIPARC:UPI000016AF9A; EMBL:Y13472; NID:g3135791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-1379 <POP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Gene: F1B16.6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                 ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CYSVYG---TTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                         25 DIILECVYCKQQLLRR-----EVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 YDFAFRDLC--IVYRDGNPYAVXD---KCLKFYSKISE------YRHY 79
                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 8.9%; Score 74; DB Similarity 24.3%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                     KORHLDKK---
                                                                                                       VTYCEYCQEEKTLHETVNFSGVKRPFCSEGCKLLYKQDFARRLGLRCVTCNYCSQLCKGG
                                                                                                                                                               RHYC-YSVYGTTLEQQYN-----KPLCD-----
                                                                                                                                                                                                                       DIQLKCNYCKNSFCSKPEILEWENKVHQFCSK-----TCSDDYKKLHCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOYHYONLSNOLSYNNLNPSTMSDENGKSLSVHQHHSDQILPSSVYNNNGNNGVGFYNNY
ATKELDGVVRDFCSEDCCKKFQD---
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                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                              8.9%;
                                                  ---- QRFHNIRGRW---TGRCMSCCRSSRTRRE 148
                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                              Score 74; DB Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                    Mismatches
WYYKAARC-DCCKSQGTLKE
                                                                                                                                                                                                                                                                                                                                                                                      2; Length 1379;
                                                                                                                                                            ------LIRCI--NXQKPLCPEE
                                                                                                                                                                                                                                                                                                                                    50;
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                                                                                                                                                                                                                                                                                                                                    64;
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                                                                                                          739
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A;Cross-references: UNIPROT:Q89370; UNIPARC:UPI00000F6AD8; EMBL:U42580; NID:g4028896; A;Experimental source: specific host Chlorella strain NC64A C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data A; Reference number: Z18806 A; Accession: T17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proline-rich protein A35L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #text_change 31-Dec-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004
C;Accession: A772220
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A; Residues: 1-549 < GRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9X221; UNIPARC:UPI00000C1227; GB:AE001810; GB:AE000512; A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-357 < ARN>
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Best Local S
Matches 29
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Best Local Similarity
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146 RQIQAEAEGKAAAEFQGEYRNCLLYSRYKEPPQV
                                             122 KORFHNIRGR----WTGRCMSCCRSSRTRRETOL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ALEYADRNLYDIAHDIIKFMLDIDENYAPAYELKGSLLVEQ 144
                                                                                                                                     67 LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLI----RCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                  36 TEEEQTLYQYYCKATDMYPKDTEWESKCEDLAYKYPELKLRHDMCNLWQDEYFCGMRDRN
                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQ 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 QERPRKLPQLCTELQTTIHDIILECVYCK-----QQLLRRE---VYDF-----AFRDL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                        EQLYPEFS----YCYDSDGNIDKTQ---PFCVKLCETTPGKCISQAE---AEERRKQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KENIMKEVOTCEKLEKVVH--LDETVYEPLIFPEFQEWLREENITPKDFKNVSLKGLYDL
                                                                                                                                                                                                                           TELQTTIHDIILEC---VYCKQQLLRREVYDFAFR-----DLCIVYRDGNPYAVXDKC 66
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                8.9%;
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                                                                                                                                                                                                                                                                             30;
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                                                                                                                                                                                                                                                                           Score 73.5; DI
Pred. No. 23;
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73.5;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                      Length 549;
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                                                                                                                                                                                                                                                                             29;
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                                                                                                                                                                                                                                                                             Gaps
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                                                                                          145
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PI

UIN

RESULT 74 JC7686

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A; Map position: 12q24-12q24
C; Keywords: cell adhesion; cytoskeleton; peroxisome; phospi
F;46-55/Region: proline rich
F;324-374/Domain: LIM metal-binding repeat homology <LIM1>
F;324-374/Domain: LIM metal-binding repeat homology <LIM2>
F;482-492/Domain: LIM metal-binding repeat homology <LIM3>
F;501-551/Domain: LIM metal-binding repeat homology <LIM4>
F;511/118,181/Binding site: phosphate (Tyr) (covalent) #stal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NyAlternate names: peroxisomal membrane protein 3
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;C;Species: Homo sapiens
(;C;Species: Homo sapiens
(;C;Species: Homo sapiens
(;C;Species: Homo sapiens
(;Species: Homo sapiens
(;Specie
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A55933
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Biochem. Biophys. Res. Commun. 283, 406-411, 2001
A;Title: Cloning and expression of activator of CREM in testis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:PXN
A; Cross-references: GDB:702105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-557 <SAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-284 < PAL>
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A; Accession: JC7686
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A; Introns: 53/3; 112/3; 168/3; 231/3
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                                                                             QLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCPEEKORHLDKKORFHNIRGRWTGRCMSCCR
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    QVVTAMGKTWHPEHFVCTHCQEEIGSRNFFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LCEEQFMSRDDYPFCMDCYNHLYANKCVACSK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGN----YCVPCFEK--EFAHYCNFCKKVITSGGTTFCDQLWHKECFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNPYAVXDKCLKFYSKISEYRHYC-----YSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCTECYS--NECSSKCFHCKRTIMPGSRKMEFKGNYWHETCFVCENCRQPIGTKPLISKE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 73; DB 21.1%; Pred. No. 14;
                                                                                                                                                                                                      8.8%;
20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoskeleton; peroxisome; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Mismatches
                                                                                                                                                           Score 73; DB Pred. No. 26; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPARC: UPI000002B0A7;
                                                                                                                                                                                                                                                                                                                               (covalent) #status
                                                                                                                                                                                             DB
26;
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                                                                                                                                                                                                                                             <u>ب</u>
                                                                                                                                                                                                                                        Length 557
RDGQPYCEKD----YHNLF 379
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                                                                                                                                                                                                                                                                                                                               predicted
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C;Species: Zea mays (maize)
C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01171; S72272
R;Ach, R.A.; Durfee, T.; Miller, A.B.; Taranto, P.; Hanley-Bowdoin, L.; Zambryski, P.C. Mol. Cell. Biol. 17, 5077-5086, 1997
A;Title: RRB1 and RRB2 encode maize retinoblastoma-related proteins that interact with A;Reference number: Z09601; MUID:97415586; PMID:9271385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: B55933
R;Salgia, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y. Biol. Chem. 270, 5039-5047, 1995
A;Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated A;Reference number: A55933; MUID:95197488; PMID:7534286
A;Description: cell cycle control; probably controls C;Superfamily: retinoblastoma-associated protein C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Medecule type: mRNA
A; Residues: 1-866 < ACH>
A; Cross-references: UNIPROT:022344; UNIPARC:UPI00000A3DFE; EMBL:AF
A; Xie, Q.; Sanz-Burgos, A.P.; Hannon, G.J.; Gutierrez, C.
EMBO J. 15, 4900-4908, 1996
A; Title: Plant cells contain a novel member of the retinoblastoma
A; Reference number: S72272; MUID:97045098; PMID:8890163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_iAlternate names: retinoblastoma susceptibility protein Rb1; retinoblastoma-related C_iSpecies: Zea mays (maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paxillin – chicken
                                                                                       C; Function:
                                                                                                        A;Gene: RRB1; Rb1
                                                                                                                                                                                                A;Molecule type: mRN
A;Residues: 184-866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G1/S transition control protein Rb1 - maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;31,118/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B55933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:P49024; UNIPARC:UPI0000131378; GB:U14589; Keywords: cell adhesion; cytoskeleton; phosphoprotein; zinc finger; 46-55/Region: proline-rich
                                                                                                                                                                                                                                                       Accession: S72272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 1-559 <SAL>
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;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
                                                                                                                                                                      Cross-references: UNIPARC:UPI000002EEEB; EMBL:X98923; NID:g1617473; PIDN:CAA67422.1;
                                                                                                                                      Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCIN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPRCYYC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCIN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVVTAMGKTWHPEHFVCTHCQEEIGSRNFFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPRCYYC--
                                                                                                                                                                                                                             mRNA
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Pred. No. 27;
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                                                       G1/S
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                                                       phase
                                                                                                                                                                                                                                                                                                                                                                                          EMBL: AF007793; NID: g2352794;
                                                          transition
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Query Match Best Local Similarity

8.7%;

Score 72.5; Pred. No. 45;

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Length

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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 (c;Accession: G82108 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio ch A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-422 <WIL>
A;Cross-references: UNIPROT:Q20082; UNIPARC:UPI000007F86E; EMBL:Z36752; PIDN:CAA85325.1;
A;Experimental source: clone F35H8
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
T21820
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A;Molecule type: DNA
A;Residues: 1-270 <HEI>
A;Cross-references: UNIPROT:Q9KQ28; UNIPARC:UPI000013B7DF; GB:AE004289; GB:AE003852; NII
A;Cross-references: serogroup OI; strain NI6961; biotype El Tor
                                                                               A; Map position: 2
A; Introns: 24/1; 52/2;
                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, August 1994
A;Reference number: Z19475
A;Accession: T21820
                                                                                                                                                                                                                                                                                                                                       C; Accession:
R; Berks, M.
                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F35H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Query Match
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Best Local S
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                                                                                                                             Gene: CESP:F35H8.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 -- IEHCPNDPAAELLKTQVN 259
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTLEQQYNKPLCDLLIRCIN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSALLREERYTLALRCTDLALTFVPDDPYEIRDRGFIYQQLQCHQIAISDYQYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YNKPLCDLLIRCINXQKPLCPEE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                 98/1; 191/3; 274/3; 368/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.7%;
8.7%; Score 72; DB
23.6%; Pred. No. 25;
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB
Pred. No. 16;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
16;
                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
43;
                                         Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
  38;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
H86477
                                                                                                                                                                                                                                                    R;Bird, A.J.; Turner-Cavet, J.S.; Lakey, J.H.; Robinson, N.J. Biol. Chem. 273, 21246-21252, 1998
A;Title: A caboxyl-terminal Cys2/His2-type zinc-finger motif A;Reference number: Z17359; MUID:98362004; PMID:9694883
A;Accession: T11850
                                                                                                                                                                                                                                                                                                                                                         C;Species: Synechococcus sp.

A;Variety: PCC 7942
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
C;Accession: T11850
                                       A;Description: interacts with DNA to synthesize the C;Superfamily: DNA primase C;Keywords: DNA replication; nucleotidyltransferase
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-616 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                         C; Function:
                                                                                                                           A; Gene:
                                                                                                                                                   C;Genetics:
                                                                                                                                                                    A; Cross-references: UNIPROT: P74893; UNIPARC: UPI00001321F0;
                                                                                                                                                                                                                              A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA primase (EC 2.7.7.-) -
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Synechococcus sp.

(PCC 7942)

from GB/EMBL/DDBJ

ä

DNA primase

influences

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71.5;

멂

2

Length

616;

primer

RNA that initiates DNA replic

EMBL: X94247

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; E ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: H86477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein F1504.19 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (nouse-ear cress) (;Species: Arabidopsis thaliana (nouse-ear cress) (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Date: 08-Mar-2001 #text_change 09-Jul-2004 C;Accession: H86477
RESULT
                                                                                                                                                                                                                                                                                         A; Gene: F1504.1
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-565 <STO:
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                              Query Match
Best Local Similarity 33...
Thes 20; Conservative
                                                                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                      Cross-references:
  81
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                                                                                                                                                                                                                                                                                                                       F1504.19
                                                                                    217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 LKDHSLLKPMFSCD--
                                                                                  VYSGVLEESSTSVTCAI---CID---DYCVGEKLRILPCKHKYHAVCIDSWLGRCRSFC
                                                                                                                                VYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI-RGRWTGRCMSCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLEQQYNKPL--CDLLIRCINXQKPLCP-----BEKQRHLDKKQRFHNIRGRWTGRCMS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYRCTNCKTYFGNKEVYQ---RHIQEVHGDARPFRCFNCGMRFANKTSMTHH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMR 262
                                                                                                                                                                                                                                                                                                                                                                         UNIPROT:Q9LQG6; UNIPARC:UPI00000A7592; GB:AE005172; NID:g8778343; PII
                                                                                                                                                                                                             33.9%;
                                                                                                                                                                                    6
                                                                                                                                                                                                             Score 71.5;
Pred. No. 3
                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                        DΒ
                                                                                                                                                                                    26;
                                                                                                                                                                                                                                     Length 565
                                                                                                                                                                                       Indels
                                                                                                                                                                                    7;
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                                                                                                                                                                                       Gaps
                                                                                    269
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; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.; Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marziali,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tallon,
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hypothetical protein SPBC31F10.14c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40217
R;Wood, V:, Rajandream, M.A.; Barrell, B.G.; Pohl, T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21913
A;Accession: T40217
                                                                                                                                                                                                                                                        RESULT 83
T40217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P21902; UNIPARC:UPI00001313DC; GB:M58366; NID:g161657; C;Superfamily: serine proteinase easter; trypsin homology C;Keywords: hydrolase; serine proteinase eyerine proteinase e;1-21/Domain: signal sequence #status predicted <SIG>
F;128-370/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A; Residues: 1-375 < MUT>
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                                    A; Residues: 1-1630 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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Matches 31; Conserv
Cross-references: UNIPROT:P87315; UNIPARC:UPI00006956C; EMBL:Z97204; PIDN:CAB10090.1 Experimental source: strain 972h-; cosmid c31F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,228,326/Active site: His, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
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                                                                                                                                                                                                                                                                                                                                                                           SCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTLEQQYNKPLCDLLIRCINXQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITASH----CVVNSAGTDVMPADVFSVRLGEHNLYSTDDDSNPIDFAVTSVKHHEHFVLA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYDFAFRDLCIVYRDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKQIPPNLPEVCGIHNTTTTRIIGGREAPIGAWPWMTAVYIKQGGIRSVQCGGALVTNRH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQERPRKLPQLCTELQTTIHDII-------LECVYCKQQLLR-----RE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HQELQRQLSRRERLYEV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERPRKLPQLCTEL--QTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXD
                                                                                                                                                                                                                                                                                                                                    FNGPSSAVLREVQL 287
                                                                                                                                                                                                                                                                                                                                                                                                                TYLN-----DIAILTLNDTVTFTDRIRPICLPYRKLRYDDLAMRKPFITG-W-GTTA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAKQFY----YCFSCGAGGNPIKFLMELGKQSFSEVVLDLAKRYQVPVRTLEVQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCLKFYSKISEYRHYCYS--VYGTTL-----EQQYNKPLCDLL-----IRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTPRLHPETIAAVKERADIVDIVSE-----QVVLKKRGKDFV--GLCPFHDDKSPSFTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 40;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KPLC-PEEKORHLDKKORFHNIRGRWTGRCM 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NPYAVXDKCLKFYSKISEYRHYCYSVYG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
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guanine nucleotide exchange factor unc-73a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T42739; T42740; T34427; T34430; T34426 R;Steven, R.; Kubiseski, T.J.; Zheng, H.; Kulkarni, S.; Mancillas, J.; Ruiz Morales, Cell 92, 785-795, 1998 R;Title: UNC-73 activates the Rac GTPase and is required for cell and growth cone mig A;Accession: T42739 A;Accession: T42739 A;Accession: T42739 A;Accession: T42739 A;Status: preliminary; translated from GB/EMBL/DDBJ
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D87749
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A;Gene: SPDB:SPBC31F10.14c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology. A;Reference number: A75000; MUID:9969613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D87749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein unc-73b (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004; Accession: D87749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: unc-73b
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les 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 --SKISEYRHYCYSVYGTT-----LEQQYNKP-LCDLLIRCINX----QKPLCPEEKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQQLLR-----REVYD---FAFRDLC---IVYRDGNPY---AVXDKCLKFY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVESMLRPRKLEPPFYLQQCWGKIFKKKFTTICERIESTLHELV-----KASLQTPEVF 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQDPQERPRKL----
                                                                                                                                                                                                                                                                                                                                                    KHMDYKERFGKGCTYALRNGDFLLRYIRR-STVNQSERKRHETKI 1035
                                                                                                                                                                                                                                                                                                                                                                                                 RHLDKKORF-----HNIRG-----RWTGRCMSCCRSSRTRRETQL 151
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22.8%; Pred. No.
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Pred. No. 1.2e+02;
Pred. No. 52;
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C97723
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                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-615 <KUR>
A;Cross-references: UNI
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A;Residues: 'MVIKCFT',1568,'LRK',1572-2488 <DU3>
A;Cross-references: UNIPARC:UPI000002A2LD; EMBL:
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submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55C7
A;Reference number: Z21524
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A;Residues: 1-2488 <DUZ>
A;Residues: 1-2488 <DUZ>
A;Cross-references: UNIPARC:UPI0000611F8; EMBL:U80436;
A;Experimental source: strain Bristol N2; clone F55C7
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A;Cross-references:
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;Residues: 1-1634,'QN',1637,'E' <ST2>
;Cross-references: UNIPARC:UPI000002A21C; EMBL:AF048835;
                                                                                            ;Gene: aspS
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    Query
                                                                    Superfamily: lysine-tRNA
                                                                                                                    Genetics:
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Best Local
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2262/2; 2331/1;
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                                                                                                                                         UNIPARC: UPI0000164BE8;
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    8.5%;
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Pred. No. 1.7e+02
    Score
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clone F55C7
                                                                                                                                       GB:AE006914; PIDN:AAL02725.1; PID:g15619236;
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    615;
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RESULT 87
C86496
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                                                                                                                                                                                                                                                                                                                                              nypothetical protein - Chlamydophila pneumoniae (strain CV
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_C;Accession: D72127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86496
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C;Accession: CB6496
R;Shirai, M.; Hirakawa,
                                                                                                                                              A; Experimental C; Genetics:
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A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CPj0041 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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                                                                                                                             A;Gene:
                                                                                                                                                                                                                                                                                                          R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-449 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                             CPn0041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                      l Similarity
27; Conserv
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                  REVYDFAFRDLCIVYR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVYDFAFRDLCIVYR-----DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYSKISEYRHYCYSVYGTTL---EQQYNKPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVVDRFMRTTCNIRKIAMTFDRHVYSVAKTA---FEKAFGALETC--VY-ESMRESYRE
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                                                        Conservative
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                                                                       8.48;
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                                                    Score 70; DB
Pred. No. 42;
13; Mismatches
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Pred. No.
-DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Tabuchi, M.; Kishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI00000D2F9A;
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42;
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                                                        Indels
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                                                                                                                                                                                                                                                                                                                             J.; Olinger, L.; Grimwood,
                                                                                                                                                                                    GB:AE001589;
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A;Residues: 1-708 <WIL>
A;Cross-references: UNIPROT:O62305; UNIPARC:UPI000017A3A1; EMBL:Z70279; PIDN:CAA94244.1;
A;Experimental source: clone K11E8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A81544

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: A81544
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wild, A.
submitted to the EMBL Data Library,
A;Reference number: Z19771
A;Accession: T23616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T23616
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T23616
                                                                                                                                                                                                                                                                 A; Map position: A; Introns: 8/2;
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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A;Experimental source: strain AR39;
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Best Local Similarity
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           401 YHPY----HC--FTNKMSNYERAAPSSHGSSTTKKIANAIADLVIR 440
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                                                                                                                                                                               23;
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                                                -NPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIR 102
                                                                                             PQKFPRNC-----VHPFTTHPYYSPKESSKKKLFFTLLFEVCPHTSRSHILLRDNTKNI 400
                                                                                                                                  PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLC----IVYRDG----
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78/2; 100/2; 124/3; 186/1; 217/3; 258/3; 286/3; 401/2;
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                                                                                                                                                                                              8.4%; Score 70; DB 2; Length 708; 21.7%; Pred. No. 64;
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HL cells
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RiBentley, D.

Bubmitted to the EMBL Data Library, April 1996
Bubmitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C15H9
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T15519
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A;Molecule type: DNA
A;Residues: 1-1436 <TET>
A;Cross-references: UNIPROT:Q9PKP1;
A;Experimental source: strain Nigg (
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C;Accession: B81704
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                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: C15H9.3
A; Map position: X
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A;Residues: 1-314 <BEN>
A;Cross-references: UNIPROT:Q18029; UNIPARC:UPI000007A22F; EMBL:U56965; NID:g1945492;
A;Experimental source: strain Bristol N2; clone C15H9
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A;Gene: TC0424
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Best Local
                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                           y Match 8.4%; Score 69.5; Local Similarity 26.3%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 8.4%; Score 70; DB 2; 1 Local Similarity 21.9%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 VRIVTQKCLREELKDLLGKTDEELKPCDLSKIQRSVCLFATSVVSLLEGRMGVSEKSSIK 462
  284 IFRGSKCL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 -- AVXDKCLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                9 PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGN------P 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDG-NPY---- 60
                                                    YAVXDKCLKFYSKISEYRHYCYSYYGTTLEQQ-YNKPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIEETVYRELGSTILQLGGLSGGITPLIDNVHKAIRQGRALSNELRQSIQLHPERRFHRL 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDRIRSLAQ-----QKTLTAALLRKLYC-----EIED-AMHEICI--EDGISPYIQDQ 402
                                                                                                           PRKTSRVSTELKVSINFIIVSMFLLVQTLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYRHYCYSVYGTTLEQQYN-----KPLCDLLIRCINXQKPLCPEEKQR-HLDKKQRFHNI 128
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                       11; Mismatches
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  -AYMVSGSALRNAIVNLILC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC:UPI0000057904; GB:AE002309; GB:AE002160; NID (MoPn)
                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----FYSKIS 74
                                                                                                              ----YNICTLYEDNNLCLFLLFIAP 283
                                                                                                                                                                                                                       31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1436;
                                                       97
                                                                                                                                                                                                                                                                              Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       31;
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                                                                                                                                                                                                                       Gaps
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RESULT
A71928
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: The sequence A;Reference number: Z21431 A;Accession: T33884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Becker, M.; Wamsley, P.; Twyman, B.; Beck, C.; Bradshaw, H. submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid H14E04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-298 <STO>
A; Cross-references: UNI
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A;Experimental source: strain Bristol N2; clone H14E04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-327 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein H14E04.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A;Gene: At2g06010
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Datc: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                        ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Gene: CESP:H14E04.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T33884
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                        Introns: 11/2; 47/1;
Superfamily: cyclin,
                             95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 VGHNFQMNAIGWKWKLTSCLGGDGVSRIRNKTTL 200
                                                                                                          122 AIVLPKRWGVTFETTSTKNGVVYDSEFILVEILDCCLVVHHASRPMCPPPPPREIFDK 179
                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 TTLEQQYNKPLCDLLIRCINXQKPLCPEEK-----QRHLDKK---QRF-----
                                                                                                                                                                                                                                                               31 VYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSV-----
                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STNNQLÝNEPTNDYHAKLV--LKPLCPERKWKFIYEPLHQEVRVLSKKIPVTRFLNLQVG
                                                                                                                                                                                                                 IYFKRFYLRQ----SFRDMC----PFLVASTALFLACKVEE--HTTLSVSSFLKNT 121
                                                                                                                                                           ----YGTTLEQQYNKP---
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        84/2; 125/1; 167/2; 181/1; 215/1; C/H/G types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%;
30.9%;
                                                                                                                                                                                                                                                                                                                                              8.3%; Score 69; DB 2; Length 327; 23.7%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                      15;
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Pred. No.
                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                           --LCDLLIRCI---NXQKPLCPEEKQRHLDKK 122
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                                                                                                                                                                                                                                                                                                                   35; Indels
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                                                                                                                                                                                                                                                                                                                      40;
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                                                                                                                                                                                                                                                                     83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PI
tumor necrosis factor receptor 1 precursor (validated) - human N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1 N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding C;Species: Homo sapiens (man) C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004 C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A602
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GQHUT1

A60231;

A38

protein

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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: A71928 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Mexberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature 397, 176-180, 1999 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric paths A;Reference number: A71800; MUID:99120557; PMID:9923682 A;Accession: A71928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outer dense fiber protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1819 CARN'
A;Cross-references: UNIPROT:Q9ZLVO; UNIPARC:UPI00000D3637; GB:AE001481; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Molecular cloning and characterization of the bovine A;Reference number: S56100; MUID:96066278; PMID:7576240 A;Accession: S56101
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A;Molecule type: mRNA
A;Residues: 1-262 «KIM»
A;Cross-references: UNIPROT:Q29438; UNIPARC:UPI0000130BD1; GB:X69514; NID:g1165005;
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RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kim, Y.; Adham, I.M.; Haack, T.; Kremling, H.; Engel, W. Biol. Chem. Hoppe-Seyler 376, 431-435, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Helicobacto
A; Variety: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cag island protein - Helicobacter pylori (strain
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1252 RNEKEKQECEKLLTPEARKFLE----KQ----RQQKDKAIKD-CLKNADPNDRAAIMKCL 1302
                                                                                                         95 PLCDLLIRCINXQKPLCPEEKQRHL------DKKQRFHNIRGRWTGRCM--SCCRSS 143
                                                                                                                                                                                                 40 REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 KFYS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 23.2
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCL 67
                                                                 GLCDLYPCCLCDVKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NXQKPLCPEEKQRHLDKKQRFH
                                                                                                                                                         RCIDELSARCLCDLYM--HPYCCCDLHPYPYCL
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%;
                                                                                                                                                                                                                                                                  8.3%;
                                                                                                                                                                                                                                             14; Mismatches
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                     Score 68.5;
Pred. No. 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
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                                                                                                                                                                                                                                                                                          Length 262;
                                                                                                                                                                                                                                                  Indels 37;
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                                                                                                                                                           CYS-----KRSRSC 65
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A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Cross-references: UNIPARC:UPI00002D398; UNIPARC:UPI00002D836; UNIPARC:UPI00001736D8;
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble R;Gray, P.W., Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 7, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re A;Reference number: A38281; MUID:91017509; PMID:2170974
A;Accession: A38281; MUID:91017509; PMID:2170974
                                                                                                                                                                                                                                                             Gene 134, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
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A;Accession: A36555
A;Molecula type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:
                                                                       R;Seckinger, P.; Vey, B.; Turcatti, G.; Wingfield, P.; I Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, A:Reference number: A60231; MUID:90292116; PMID:2113477
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends R;Kemper, O.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI000002CE11; GB:M37764 A;Note: the authors translated the codon TGG for residue R;Nophar Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; EMBO J. 9, 3269-3278, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: part of this sequence R;Schall, T.J.; Lewis, M.; I Reviel 61, 361-370, 1990
A;Title: Molecular cloning 6
A;Reference number: A34900;
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Cell 61, 351-359, 1990
A;Title: Molecular cloning (
A;Reference number: A34899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:g339744; PIDN:AAA03210.1; R;H1mmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, DNA Cell Biol. 9, 705-715, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, Genomics 13, 219-224, 1992
A;Tille: Structure of the human TNF receptor 1 (p60) gene A;Reference number: A38208; MUID:92250049; PMID:1315717
                                                   A; Reference number: A60231; A; Accession: A60231
                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-13 < KE
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A; Residues: 1-455 < NOP>
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A; Residues: 1-455 < GRA>
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A; Residues: 1-455 < F
A; Molecule type: protein
A; Residues: 41-43,'X',45-53,'X',55-57
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T.J.; Lewis, M.; Koller,
361-370, 1990
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                                                                                                                                                         P.; Dayer, J.M.
                                                                                                         NH-2-terminal
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Gydene: CBB:TMFR1

A;Gene: GDB:TMFR1

A;Gene: GDB:TMFR1

A;Cross-references: GDB:125913; OMIM:191190

A;Map position: 12p13.2-12p13.2

A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1

C;Superfamily: tumor necrosis factor receptor type 1 (TWFR1); NGF receptor repeat homol C;Keywords: duplication; glycoprotein; receptor; transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: NGF receptor repeat protein 1 (tumor necrosis factor alpha inhibitor) #status F:44-82/Domain: NGF receptor repeat homology <NG1>
F;44-82/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;121-204/Domain: NGF receptor repeat homology <NG3>
F;121-204/Domain: transmembrane #status predicted <NEM>
F;212-35/Domain: transmembrane #status predicted <INT>
F;335-455/Domain: cransmembrane #status predicted <INT>
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F;335-455/Domain: cransmembrane #status predicted <INT>
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A;Residues: 41-43,'X', 45-53,'V', 55-57,'XK',60 <01
A;Cross-references: UNIPARC:UPI00001736E2
A;Experimental source: renal failure patient urin
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding prote:
A;Reference number: A35010; MUID:90110215; PMID:;
A;Accession: A35010
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A;Residues: 41-53, X',55-144, X',146-150, X',152-186, X',188-201
A;Cross-references: UNIPARC:UPI00001736E4
A;Experimental source: urine
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A,Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A,Reference number: JC2404; MUID:95128033; PMID:7765720
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R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 41-45 < ENG>
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A;Residues: 41-60 <GAT>
A;Cross-references: UNIPARC:UPI00001736E1
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                                                           LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRR 147
                                                                                                                                                                                           LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
                                                                                                                             LSCSKCRKEMGQVEI-----SSCTVDRD----
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25.0%;
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RESULT 100
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A;Title: sry h-1, a new Drosophila melanogaster multifingered protein gene showing lA;Reference number: A30817; MUID:89039875; PMID:3141791
A;Accession: A30817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serendipity (sry h-1) locus protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
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A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28260
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0005642
A;Introns: 338/2; 740/1
C;Keywords: DNA binding; transcription regulation; zinc finger
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A; Residues: 1-868 < VIN>
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C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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A; Residues: 1-519 < AFO>
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Matches 26; Conserv
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                                                                                                                                                           114 - EKQRHLDKKORFHNIRGRWTGRCMSCCRSSRTRR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 LYDISSENFNRIFQLCNEMSISIMELYALCAVSPKQCISVLINDTNI-NVNIV---GNKY
                                                                                                                                                                                                                                                          65 KCLK-----FYSKI-SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPL-CPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AVXDKCL----KFYSKISEYR------HYCYSVYGTTLEQ-----QYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                         FQERSHLQRHQKYHAQTRSY--RCEKCGKMYKTER 426
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Pred. No. 66;
19; Mismatches 54;
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skeletal muscle LIM-protein SLIM1 - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004 (;Accession: JC4893; G02741 (R;Morgan, M.J.; Madgwick, A.J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 225, 632-638, 1996
A;Title: Slim defines a novel family of LIM-proteins expressed
A;Reference number: JC4893; MUID:96354835; PMID:8753811
A;Accession: JC4893
Search completed: May 27, Job time: 33.1084 secs
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A;Reeidues: 1-280 <MO2>
A;Cross-references: UNIPROT:Q9Y630; UNIPARC:UPI000017C350; EMBL:U60115; NID:gl381807; PII
F;162-212/Domain: LIM metal-binding repeat homology <LIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0042025;
GO; GO:0003677;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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DeFilippis V.R., Ayala
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Li; AJ388057; CAB45106.1; -; Genomic_DNA.
Li; AJ388065; CAB45130.1; -; Genomic_DNA.
Li; AY089951; AAM11875.1; -; Genomic_DNA.
Li; AY089954; AAM11881.1; -; Genomic_DNA.
Li; AY089954; AAM11881.1; -; Genomic_DNA.
Li; AY112663; AAM51854.1; -; Genomic_DNA.
GO:0042025; C:host_cell_nucleus; IEA.
GO:003677; F:DNA_binding; IEA.
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Q89852 9PAPI
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J. Virol.
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EMBL; U34127; AAA91674.1; -; Genomic_DNA.
EMBL; U34133; AAA91680.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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01-NOV-1996, sequence version
07-FEB-2006, entry version 25.
Early transforming protein E6.
                                        Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                              Human papillomavirus type Viruses; dsDNA viruses, no
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07-FEB-2006,
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae.
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Viruses; dsDNA viruse
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Virol. 69:7743-7753(1995).
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Pred. No. 2.4e-73;
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RESULT 4
QSWMP5 HPV16
ID QSWMP5 HPV16
AC QSWMP5;
DT 01-NOV-1999, 1
DT 07-FEB-2006, 0
DE E6 protein.
OS Human papillom
OC Viruses dsDNI
OC Alphapapillom
OX NCBI TAXID=33
RN [1]
RP NUCLEOTIDE SE
RP MUCLEOTIDE SE
RP MEDLINE=20112;
RA Verheijen R.H
RT "Analysis of 1
RT p53 codon 72 |
RL J. Gen. Virol
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Matches 149
                  NUCLEOTIDE SEQUENCE.
MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst
van Duin M., Snijders P.J., Vossen M.T., Walboomers J.M.;
verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
vanalysis of human papillomavirus type 16 E6 variants in relatio
paga codon 72 polymorphism genotypes in cervical carcinogenesis.
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.
J. Gen. Virol. 81:317-325(2000).
                                                                                                                                                                                                                                                    01-NOV-1999, integrated int
01-NOV-1999, sequence versi
07-FEB-2006, entry version
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EMBL; AF486322; AAL96627.1; -; Genomic_DNA.
EMBL; AY686580; AAV91652.1; -; Genomic_DNA.
GO; GO:0042025; C:host_cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Xu L.Y., Cheng A.F.; Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                 Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on complete genome analyses.";
J. Virol. 79:7014-7023(2005).
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Pred. No. 2.5e
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 11.
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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Distributed under the Creative Commons Attribution-NoDerivs Li
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EMBL; AJ388061; CAB45114.1; -; Genomi
EMBL; AJ388066; CAB45124.1; -; Genomi
GO; GO:0042025; C:bost cell nucleus;
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                                                                                                                                            Score 823; DB 2;
Pred. No. 4.7e-73;
1; Mismatches 2
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RESULT 7

Q8BB20 HPV16

Q8BB20_HPV16 PRELIMINARY; PR

ID OBB20;

DT 01-MAR-2003, integrated into Uni

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Early transforming protein E6.

OS Human papillomavirus type 16.
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Q89755 9PAPI
Q89755;
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern
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Viruses; dsDNA viruses, no RNA stage;
unclassified Papillomaviridae.
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J. Virol. 69:7743-7753(1995).
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L; U34111; AAA91658.1; -; Genomic_DNA.
L; U34121; AAA91668.1; -; Genomic_DNA.
L; U34123; AAA91670.1; -; Genomic_DNA.
GO:0042025; C:host_cell_nucleus; TEA.
GO:0003677; F:DNA_binding; TEA.
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151 AA; 1:
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ilarity 98.0%;
Conservative
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Pred. No. 4.7e-73;
1; Mismatches 2;
                                                 UniProtKB/TrEMBL.
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36 HPV16

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D P03126; Q71B17;

T 21-JUL-1986, into

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MEDLINE=90218027; PubMed=2157796; Schneider-Maunoury S., Pehau-Arnaudet G., Bre "Expression of the human papillomavirus type a line derived from a vulvar intraepithelial J. Gen. Virol. 71:809-817(1990).
                                                                                                                                                             MEDLINE=85246220; PubMed=2990099; Seedorf K., Krammer G., Durst M., "Human papillomavirus type 16 DNA Virology 145:181-185(1985).
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Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=ISOlate European German 131;
Terai M., Fu L., Ma Z., Burk R.D.;
"Cloning and sequencing of non-European human
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Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                      Submitted (AUG-2002) to the EMBL/GenBank/DDBJ
                                                                                               variant complete PCR method.";
                                                                                                                                                                                                                                                                                            Protein E6.
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J. Mol. Evol. 55:491-499(2002).
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                                                                                                         genomes from cervicovaginal
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Pred. No. 4.7e-73;
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RESULT 9
Q547J2_HPV16
ID Q547J2_HPV16
AC Q547J2_T
DT 24-MAY-2005, s
DT 24-MAY-2005, s
DT 24-MAY-2006, e
DE Transforming p
GN Name=E6;
OS Human papillom
OC Viruses; dsDNA
OC Alphapapilloma
OX NCBI_TaxID=333
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ZN_FING
MOTIF
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EMBL; AF536179; AAQ10712.1; -; Genomic_DNA
EMBL; D00735; BAA00632.1; -; Genomic_DNA.
PIR; A03682; WGWLHS.
PDB; 2FK4; NMR; A=87-158.
InterPro; IPR001334; E6.
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"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
Biochem. Biophys. Res. Commun. 296;962-969 (2002).
-I- FUNCTION: Transcriptional transactivator. Binds double stranded
Viruses; dsDNA viruses, Alphapapillomavirus. NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                              Human papillomavirus type 16
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Nuclear protein; Oncogene; Transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBCELLULAR LOCATION: Nuclear matrix-associated.
SUBCELLANEOUS: HPV16, in comparison to HPV types 6
Often associated with malignant genital cancers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
protein ligase, the human TP53/p53 tumor suppressor protein by
targeting it to degradation. Binds and targets human MUPP1/MPDz
protein to degradation. Those two functions presumably contribute
to transforming activity (By similarity). Interaction with human
FBLN1 protein also seems to be linked to cell transformation.
SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which
interacts with human P53. Binds to human FBLN1 and MPDZ (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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                                                                            sequence version entry version grotein E6.
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98.0%;
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                              RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 823; DB 1;
Pred. No. 4.9e-73
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R -> G (in Ref. 2).
L -> V (in Ref. 2).
; 01FEF5ADCFDB37EB CRC64;
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RESULT 10
Q919C6 HPV16
ID Q919C6 HPV16
AC Q919C6;
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EMBL; AY686581;
GO; GO:0042025;
GO; GO:0003677;
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NUCLEOTIDE SEQUENCE.
STRAIN=E-P, E-G24IT, E-G187T, and E-G538T;
STRAIN=22183962; PubMed=12195358; DOI=10.1086/342048;
MEDLINE=22183962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
                     Human papillomarirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                    01-DEC-2001, integrated into U
01-DEC-2001, sequence version
07-FEB-2006, entry version 16.
E6 protein (Fragment)
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EMBL;
EMBL;
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PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
Chen Z., Terai M., Fu L., Herroro R., DeSalle R., Burk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on complete genome analyses.";
J. virol. 79:7014-7023(2005).
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Submitted (APR-2002) t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Z., Terai M., Fu L., Herrero R., DeSalle R., Burk R.D.;
"Diversifying selection in human papillomavirus type 16 lineages based
NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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L; AF486311; AAL96617.1; -; Genomic_DNA.
L; AF486313; AAL96618.1; -; Genomic_DNA.
L; AF486317; AAL96622.1; -; Genomic_DNA.
L; AF486320; AAL96625.1; -; Genomic_DNA.
L; AF486321; AAL96625.1; -; Genomic_DNA.
L; AF486321; AAL96626.1; -; Genomic_DNA.
L; AF486321; AAM29167.1; -; Genomic_DNA.
L; AY098919; AAM29160.1; -; Genomic_DNA.
L; AY088581; AAV91660.1; -; Genomic_DNA.
GO:00042025; C:host_cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0003677; F:DNA binding; IEA.
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 4.9e-73;
1; Mismatches 2
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
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QBBB19;
Q1-mAR-2003, integrated into U
01-mAR-2003, sequence version
07-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                   EMBL; AY089955; AAM11883.1; -; Genomic DN
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InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=2224222; PubMed=12355268; DOI=10.1007/800239-002-2344-y; DeFilippis V.R., Ayala F.J., Villarreal L.P.; "Evidence of diversifying selection in human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF404697; AAL01351.1; -; Genomic_DNA.
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GO; GO:0003677; F:DNA binding; IEA.
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cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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Evol. 55:491-499(2002).
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ilarity 98.0%;
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                                                                                                                                                Score 821; DB 2; Length 1: Pred. No. 7.4e-73; Indels 1; Mismatches 2; Indels
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RESULT 13
Q8QRD7_HPV16
ID Q8QRD7;
AC Q8QRD7;
DT 01-UUN-2002, s
DT 01-UUN-2002, s
DT 07-FEB-2006, e
DE E6 protein.
OS Human papillom
OC Viruses; dsDNA
OC Alphapapilloma
OX NCBI_TAXID=333
RN [1] TAXID=333
RN NUCLEOTIDE SEQ
RC STRAIN=E-C442T
RX MEDLINE=221829
RA Cheung J.L.K.,
RT "Human papillo
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STRAIN=E-C442T;
MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chann P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
                                                                                                              Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Qv18158E;
STRAIN=Qv18158E;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Z., Terai M., Fu L., Herrero R., DeSalle R., Burk R.D.; "Diversifying selection in human papillomavirus type 16 lineages based on complete genome analyses."; J. Virol. 79:7014-7023(2005).
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Human papillomavirus type 16.
Human papillomaviruses, no RNA stage; Papillomaviridae;
                                                                         NUCLEOTIDE SEQUENCE
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QBQRDB HPV16 PRELIMINARY; PRT; 158 AA.
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Q1-UN-2002, integrated into UniProtKB/TrEMBL.
O1-UN-2002, sequence version 1.
O7-FEB-2006, entry version 13.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:NMA binding; IEA.
erPro; IPR001334; E6.
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NCE 158 AA; 19173 MW;
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AA; 19188 MW;
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Pred. No. 9.8e-73;
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EMBL; AF003018; AAB70735.1; -; Genomic_DN,
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI TaxID=333760;
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J. Gen. Virol. 78:2199-2208(1997).
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Pred. No. 1.2e-72;
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NUCLEOTIDE SEQUENCE.
MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern ;
Jenison S.A.;

papillomavirus

type 16 variant lineages Halpern A.L.,

Stewart A.C., Hildesheim

A

in United States

Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage;
unclassified Papillomaviridae.

Papillomaviridae

NCBI_TaxID=10566;

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RESULT 17

Q89648 9PAPI
Q89648; O12653; O12654; O12928; O12929;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 21.
DT 07-FEB-2006, entry version 21.
DT 07-FEB-2016, entry version 21.
DE Early transforming protein E6.
OC Viruses; dsDNA viruses, no RNA stage; Papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomavirus cunclassified Papillomaviridae.
OC Viruses; dsDNA viruses, no RNA stage; Papillomavirus Cunclassified Papillomaviridae.
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Matches 147
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EMBL; AF469198; AAA015693.1; -; Genomic_DNA.
EMBL; U34115; AAA91662.1; -; Genomic_DNA.
EMBL; U34129; AAA91667.1; -; Genomic_DNA.
EMBL; U34124; AAA91671.1; -; Genomic_DNA.
EMBL; U34124; AAA91671.1; -; Genomic_DNA.
CO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                     Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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NCE 151 AA; 18348 MW;
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             KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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RESULT 18
Q9W931_HPV16
ID Q9W931_HPV16
AC Q9W931_
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EMBL; U34113; AAA91660.1; -; Genomic_DNA.
EMBL; U34113; AAA91660.1; -; Genomic_DNA.
EMBL; U34135; AAA91682.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PP00518; E6; 1.
SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ388059; CAB45110.1; -; Genomic_DNA.
EMBL; AJ388058; CAB45108.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003577; F:DNA binding; IEA.
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MEDLINE=20112892; PubMed=10644829;
Van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
Van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation
"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18306 MW;
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147; Conserv
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                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFQDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                    Score 819; DB -,
pred. No. 1.2e-72;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     6FB3D9E0F24A5300 CRC64;
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Q2DJN9 HPV
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DT 24-JN
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E6 pr
GN Name=
OS Humann
OC Virus
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OX NCBI
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RN WICLE
RA Mirsh
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                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.

STRAIN-As-P, As-C193, and As-A178;

MEDLINE-22182962; PubMed-12195358; DOI=10.1086/342048;

MEDLINE-22182962; PubMed-12195358; DOI=10.1086/342048;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K.,

Cheung J.L.K., Xu L.Y., Cheng A.F.;

"Human papillomavirus type 16 intratypic variant infection cervical neoplasia in southern China.";
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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07-FEB-2006,
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Q2PJN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alphapapillomavirus.
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                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                               Terai M., Fu L., Ma 2., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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pred. No. 1.2e-72;
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Q1-NOV-1996, i
01-NOV-1996, g
07-FEB-2006, g
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EMBL;
                                                                                                                                                                                                                                                                                         EMBL; U34122; AAA91669.1; -; Genomic-
GO; GO:0042025; C:host cell nucleus;
GO; GO:0003677; F:DWA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human papillomavirus type 16 variant lineages in United populations characterized by nucleotide sequence analysis L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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Human papillomavirus.
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GO; GO:0003677; F:DNA bi
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MEDLINE=96079021; PubMed=7494284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.
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SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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AF486302;
AF486306;
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AF534061;
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F:DNA binding; IEA.
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STRAIN-E-G276T, and E-G276G442T;

STRAIN-E-G276T, PubMed=12195358; DOI=10.1086/342048;

MEDIJINE=22182962; PubMed=12195358; DOI=10.1086/342048;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheung A.F.;

Cheung J.L.K., Xu L.Y., Cheng A.F.;

"Human papillomavirus type 16 intratypic variant infection for cervical neoplasia in southern China.";

J. Infect. Dis. 186:696-700(2002).
Viruses; dsDNA viruses, no RNA stage; unclassified Papillomaviridae. NCBI TaxID=10566;
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EMBL; AF486333; AAL96628.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:NNA binding; IEA.
InterPro; IPR001334; E6.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
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01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 13.
                                                                                                                                                                        E6 protein
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nilarity 97.4%;
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Pred. No. 1.5e-72;
2; Mismatches 2; Indels
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EMBL; AJ388062; CAB45116.1; -; Genomic_DNA.
EQ; GQ:0042025; C:host cell nucleus; IEA.
EQ; GO:0003677; F:DNA binding; IEA.
InterPro; IRR001334; E6.
Pfam; PF00518; E6; 1.
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MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
varheljen R.H., Helmerhorst T.J., Meljer C.J., Walboomers J.M.;
verheljen R.H., Helmerhorst T.J., Meljer C.J., Walboomers J.M.;
nanlysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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NCBI_TaxID=333760;
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Viruses; dsDNA viruses, no
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                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18348 MW;
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Q919D4;
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Q8QRD9;
01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 14.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheng A.F.;
                                                                                                              STRAIN=A8-A267
                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 16.
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PF00518; E6; 1.
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J. Infect. Dis. 186:696-700(2002).
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 1917
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Pred. No. 2.4e-72;
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01-MAY-2000,
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EMBL; AF486305; AAL96601.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 19187 MW; 155BF5ADCE6B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and for cervical neoplasia in southern China.";
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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Lee H.P., Song Y.S.,
Submitted (SEP-1999)
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_HPV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect. Dis. 186:696-700(2002).
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                                                                                                                                                                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                     KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                           AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKFLCDLLIRCINCQKFLCFDEKQRHLD
                                                                                                                                                                                                                                                             MFQDPQERPRKLPQLCTELQTTIHEIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                             Conservative
 Papillomaviridae.
                                                                         integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       98.3%;
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                                                                                                                                                                                                                                                                                                         Score 816; DB
Pred. No. 2.4e-
3; Mismatches
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                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                            155BF5ADCE6B36F0 CRC64;
            stage;
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                                                                                                                                                                                                                                                                                                       e 816; DB 2; Lei
1. No. 2.4e-72;
                                                                                                 151
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              Papillomaviridae;
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Best Local S
Matches 147
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SEQUENCE
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RESULT 30
Q8QRD5 HPV16
ID Q8QRD5;
DT 01-UUN-2002, i
DT 01-UUN-2002, i
DT 01-UUN-2002, i
DT 01-FEB-2006, e
DE Transforming p
OS Human papillom
OC Viruses; dsDNA
OC Alphapapillom
OC NCBI TaxID=333
RN [1]
RP NUCLEOTIDE SEC
RC STRAIN=NA1;
RX MEDLINE=221829
RA Cheung J.L.K.,
RT "Human papillo
RA Cheung J.L.K.,
RT "Human papillo
RA Cheung J.L.K.,
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RA Cheung J.L.K.,
RT "Human papillo
RA CHEUNG STRAIN-2015351
RX STRAIN=QV15351
RX PubMed=1589094
RA Chen Z., Terai
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EMBL; U34107; AAA91654.1; -; Genomic_DNA.
EMBL; U34112; AAA91659.1; -; Genomic_DNA.
EMBL; U34116; AAA91663.1; -; Genomic_DNA.
EMBL; U34119; AAA91666.1; -; Genomic_DNA.
EMBL; U34119; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
NUCLEOTIDE SEQUENCE.
STRAIN=Qv15351AA, and Qv15321AA;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
PubMed=15890941; Market Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route Route
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming protein E6.
Human papillomavirus type 16.
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J. Virol. 69:7743-7753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jenison S.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10566;
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ilarity 97.4%;
Conservative
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; 18355 MW;
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Pred. No. 2.9e-72;
1; Mismatches 3;
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                Burk R.D.;
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s of the
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RESULT 31

QBQRD6 HPV16 PRELIMINARY; PRT; 158 AA.

AC QBQRD6;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.

DT 07-PEB-2006, entry version 13.

DE E6 protein.

OS Human papillomavirus type 16.

CV Viruses; dsDNA viruses, no RNA stage; Papillomav OC Alphapapillomavirus.

OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.

RC STRAIN=E-T360T;
RC STRAIN=E-T360T;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., L. RA Cheung J.L.K., Xu L.Y., Cheung A.F.;

"Human papillomavirus type 16 intratypic variant
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Best Local Sim
Matches 147;
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EMBL; AY686582; AAV91668.1; -; Genomic_DNA.
EMBL; AY6402678; AAV91668.1; -; Genomic_DNA.
EMBL; AY098923; AAM29171.1; -; Genomic_DNA.
EMBL; AY112662; AAM29171.1; -; Genomic_DNA.
EMBL; AY112662; AAM21853.1; -; Genomic_DNA.
EMBL; AY686579; AAV91644.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 19208 MW; B8E47F57F22EC2E
     MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and
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Cruz M.R., Martins C.
Submitted (MAY-2002)
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Terai M., Burk R.D.;
Submitted (JUL-2001)
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SEQUENCE
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF187869; AAF13398.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
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AA; 19210 MW;
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OBORE1;
O1-JUN-2002, integrated into UniProtKB/TrEMBL
O1-JUN-2002, sequence version 1.
O7-FEB-2006, entry version 14.
                                         MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheng A.F.; Cheung J.L.K., Xu L.Y., Cheng A.F.; Cheng A.F.; The Man papillomavirus type 16 intratypic variant infection for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                           Human papillomavirus type 1 Viruses; dsDNA viruses, no Alphapapillomavirus.
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MEDLINE-21846229; PubMed-11857370; DOI=10.1002/ijc.10103;

MEDLINE-21846229; PubMed-11857370; DOI=10.1002/ijc.10103;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type cervical cancer isolates from Australia and New Caledonia.";
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
NCBI TaxID=333760;
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                                                                                                                                     STRAIN=As-C131
                                                                                                                                                                                                                                        E6 protein
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GO:0042025; C:host cell nucleus; IE
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
m; PF00518; E6; 1.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
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Pfam; PFO
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J. Gen. Virol. 78:2199-2208(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A.,
Beth-Giraldo E., Giraldo G.,
"Sequence variations and viral genomic state
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Pred. No. 5.7e-72;
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Q9WMP4 HPV16
Q9WMP4;
Q9WMP4;
Q1-NOV-1999, integrated into
Q1-NOV-1999, sequence version
Q1-PEB-2006, entry version 10
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012336;
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                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 16. Viruses; dsDNA viruses, no RN Alphapapillomavirus. NCBI_TaxID=333760;
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                         MEDIINE=97437474; PubMed=9292007; Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro Beth-Giraldo E., Giraldo G.; "Sequence variations and viral genomic state of human type 16 in penile carcinomas from Ugandan patients."; J. Gen. Virol. 78:2199-2208(1997).
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                                                      Distributed under the Creative Commons Attribution-NoDerivs License
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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NCE 151 AA; 18387 MW;
     AF003016;
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Pred. No. 7.2e-72;
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O2ODH7;
O1-MAY-2000, integrated into Unit
O1-MAY-2000, sequence version 1.
O7-FEB-2006, entry version 17.
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GO; GO:0003577; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18206 MW; 51C12/
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 19215 MW; FC5BF2B06576864B CRC64;
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Pred. No. 1.2e-71;
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Pred. No. 9e-72;
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158
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                                                                                                                                                                                                                                                                                                                                                              Length 158
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                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 39
QBBB21 HPV16
ID QBBB21 HPV16
AC QBBB21;
DT 01-MAR-2003, i
DT 01-MAR-2003, i

PRELIMINARY;

151

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integrated into UniProtKB/TrEMBL
sequence version 1.

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Query Match
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Q9WMP2;
01-NOV-1999;
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                                                                       InterPro;
Pfam; PF00
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.

MEDLINE-20112892; PubMed-10644829;

WEDLINE-20112892; PubMed-10644829;

van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation

p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

J. Gen. Virol. 81:317-325(2000).
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                                                                                                                   EMBL; AJ388067; CAB45126.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
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                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999, sequence version 07-FEB-2006, entry version 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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HPV16
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Evol. 55:491-499(2002).
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                                              ; IPR001334; E6.
00518; E6; 1.
151 AA; 18306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integrated into UniProtKB/TrEMBL.
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protein E6.
                                                   18306 MW;
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  97.3%;
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Pred.
  Score
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                                                   5E71B4EF44993C34 CRC64;
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No. 1.4e-71;
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DB
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Length
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RESULT 42
Q76TSO_9PAPI
ID Q76TSO_9PAPI
AC Q76TSO;
DT 05-JUL-2004,
DT 05-JUL-2006,
DE Early transfo
OS Human papillor

integrated PRELIMINARY;

into

UniProtKB/TrEMBL

151

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05-JUL-2004, integral of JUL-2004, sequent of FEB-2006, entry versely transforming party
entry version 11.

E6

papillomavirus

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Q919A9 HPV16
ID Q919A9 H
AC Q919A9 H
AC Q919A9 H
DT Q1-DEC-2
DT Q1-DEC-2
DT Q1-DEC-2
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Best Local
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Q919A9;
01-DEC-2001, integrated into Uni
01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 16.
E6 protein (Fragment).
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SEQUENCE
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Viruses; dsDNA viruses, no RI
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF404706; AAL01368.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. J. Cancer 97:868-874(2002).
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                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=333760;
131
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Submitted
[3]
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                                                                                                                     MUCLEOTIDE SEQUENCE: MUCLEOTIDE SEQUENCE: PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
                                                                                                                                                                                                                                                                                                             Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
MCBI_TaxID=333760;
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EMBL; U34125; AAA91672.1; -; Genomic_DNA.
EMBL; U34130; AAA91677.1; -; Genomic_DNA.
EMBL; U34131; AAA91678.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003577; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                         NUCLEOTIDE SEQUENCE.
Terai M., Ma Z., Burk
Submitted (JAN-2002) t
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unclassified Papillomaviridae.
NCBI_TaxID=10566;
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151 AA; 18292 MW;
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Best Local Similarity
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF003014; AAB70731.1; -; Genomic EMBL; AF003017; AAB70734.1; -; Genomic EMBL; AF072508; AA015697.1; -; Genomic EMBL; AJ388068; CAB45128.1; -; Genomic EMBL; AF003013; AAB70730.1; -; Genomic GO; GO:00042025; C:host cell nucleus; IE GO; GO:0003677; F:DNA binding; IEA. InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                              LT 44
UB HPV16
QBJMUB HPV16
QBJMUB;
                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
Terai M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002, integrated into UniProtKB/TrEMBL 01-OCT-2002, sequence version 1. 07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relation p53 codon 72 polymorphism genotypes in cervical carcinogenesis. J. Gen. Virol. 81:317-325(2000).
                                                             EMBL; AV098922; AAMZ9170.1; -; Genom.
EMBL; AF556180; AAQ10720.1; -; Genom.
GO; GO:0042025; C:hoet cell nucleus;
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                  Cruz M.R., Cerqueira
Martins C.R.F.;
                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                           Transforming protein E6.
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Distributed
                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 16.
                                         Pfam;
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                                                                                                                                                                                                                                                                                      NCBI_TaxID=333760;
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                                     Pro; IPR001334; E6. PF00518; E6; 1.
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NCE 151 AA; 18292 MW;
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Pred. No. 2
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ucleus; IEA.
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                          CB70F51C00F867DC CRC64;
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Length 158;
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RESULT 46
Q89708_9PAPI
ID Q89708_9PAPI
AC Q89708;
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E16 HPV16
PRELIMINARY; PR
Q77E16;
Q77E16;
05-JUL-2004, integrated into Uni
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 11.
E6 oncoprotein (E6 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voor Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers "Analysis of human papillomavirus type 16 E6 variants in r p53 codon 72 polymorphism genotypes in cervical carcinogen J. Gen. Virol. 81:317-325(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ponglikitmongkol M., Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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L; AJ388063; CAB45118.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0003677; F:DNA binding; IEA.
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nilarity 96.0%;
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2; Mismatches
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                               PRT;
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  RESULT 47

Q9MMP3 HPV16

ID Q5MMP3 H

AC Q9MMP3-1

DT 01-NOV-1

DT 01-NOV-1

DT 07-FEB-2

DE E6 prote-
OS Human pa

OC Viruses;
OC Alphapap

OX NCBL Tax

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NCBI_TaxID=10566;
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EMBL; U34128; AAA91675.1; -; Genomic_DNA.
EMBL; U34117; AAA91664.1; -; Genomic_DNA.
EMBL; U34118; AAA91665.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; OF312A8BDBA66
                                     MEDIINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Voseen M.T., Klaassen E., Voorhorst Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relatip53 codon 72 polymorphism genotypes in cervical carcinogenesis. J. Gen. Virol. 81:317-325(2000).
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Pred. No. 3.5e-71;
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EMBL; AP472509; AAO15705.1; -; Genomic_DNA.
EMBL; AP486324; AAL96629.1; -; Genomic_DNA.
EMBL; AY098918; AAM29166.1; -; Genomic_DNA.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:000477; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Terai M., Ma Z., Bur
Submitted (JAN-2002)
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MEDLINE=22102962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., C
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
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01-JUN-2002, sequence version
07-FEB-2006, entry version 13.
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Human papillomavirus type 16.
Viruses; daDNA viruses, no RN
Alphapapillomavirus.
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002) to the EMBL/GenBank/DDBJ databases
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                       96.9%;
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                       Score 804; DB 2;
Pred. No. 3.7e-71;
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                                               Length 158;
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RESULT 50

Q919C4 HPVI6
ID 2919C4;
ID 2919C4;
AC Q919C4;
DT 01-DEC-2001, integrated into Uni
DT 01-DEC-2001, sequence version 1.
DT 07-EEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dabNA viruses, no RNA s
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
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Q9QDH5_HPV
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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   NUCLEOTIDE SEQUENCE.
MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
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                                                                                                                                                                                                                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 4.7e-71;
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                                                                 stage;
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                                                                 Papillomaviridae;
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RESULT 51
Q91986_HPV16
ID Q91986;
AC Q91986;
DT 01-DEC-2001, s
DT 01-DEC-2001, s
DT 07-FEB-2006, e
DT 07-FEB-2006, e
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Best Local S
Matches 140
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Best Local Similarity
Matches 139; Conserv
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papilloma cervical cancer isolates from Australia and New Caledonia Int. J. Cancer 97:868-874(2002).
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L; AF404702; AAL01361.1; -; Genomic_DN GO:0042025; C:host cell nucleus; IEA. GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                        Score 774; DB 2;
Pred. No. 3e-68;
1; Mismatches
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Pred. No. 6.2e-69;
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RESULT 53
Q919C0_HPV16
ID Q919C0,
AC Q919C0,
DT 01-DEC-2001, a
DT 01-DEC-2001, a
DT 07-FEB-2006, e
DT 07-FEB-2010
DT 07-FEB-2011 on
OC Viruses; dsDNA
OC Albhapapillom
OC Viruses; dsDNA
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01-DEC-2001, sequence versi
07-FEB-2006, entry version
E6 protein (Fragment).
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  NUCLEOTIDE SEQUENCE.
MEDIJNE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papilloma:
                                                                                                                                                             Viruses; dsDNA viruses, Alphapapillomavirus.
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Viruses; dsDNA viruses, no RNA
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Pred. No. 2.8e-66;
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RESULT 54

Q919C2 HPV16

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Matches 128
                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                              Matches
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pf4am; PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001, sequence version 07-FEB-2006, entry version 16. E6 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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GG:0042055; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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  61
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SVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR
                                                                                                                            TIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCY
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                                                                                                                                                                                                                                                                                             130 AA;
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                                                                                                                                                                                                                                                                                             15779 MW;
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                                                                                                                                                                                              .
                                                                                                                                                                                                                     Score 712; DB 2;
Pred. No. 3.6e-62;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                             26D0147D396B0929 CRC64;
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RESULT 56
Q919C8_HPV16
ID Q919C8 HPV16 PRELIMINARY; PR
AC Q919C8;
DT 01-DEC-2001, integrated into Uni
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA s
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Q91988 HPV16 PRELIMINARY; PRT;
Q91988;
01-DEC-2001, integrated into UniPr
01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF404701;
GO; GO:0042025;
GO; GO:0003677;
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
NUCLEOTIDE SEQUENCE.

MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;

Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874 (2002).
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                                                                                                                                                                                                                                                                                                          Alphapapillomavirus.
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                                                                                                                                                                                                                                                   NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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042025; C:host cell nucl
003677; F:DNA binding; I
C:IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYAVXDKCLKFYSKISEYRHYCYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCWSCCRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRS 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrated into UniProtKB/TrEMBL
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98.4%;
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                                                                                                                                                                                                                                                                                                                                         RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 707; DB 2;
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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cleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92D3C07BF96B092F CRC64;
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RESULT 57
Q91984_HPV16
ID Q91984;
AC Q91984;
DT 01-DEC-2001, integrated into Uni
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
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Best Local S
Matches 126
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Best Local :
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                                                                                                                                                                                                                                                                    WALLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Coseart Y.E., Rose B.R.; "Sequence variation and physical state of human papilloma cervical cancer isolates from Australia and New Caledonia
                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
                                                                                                                                            NON TER
                                                                                                                                                                                  EMBL; AF404703; AAL01363.1; -; Genomic_DN
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF404696; AAL01349.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003577; F:DNA binding; IEA.
                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                          protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
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                                                                                                                                                                Pro; IPR001334; E6.
PF00518; E6; 1.
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127; Conserv
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                                                                                                                                                                                                                                                           Cancer 97:868-874(2002).
                                                                                                               Similarity
                                                                     TIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCY
                               SVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR
                                                            TIHNIILECVYCKQQLLRKEVYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISEYRHYCY
SSRTRRETQL
                   SLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIHNIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISEYRHYCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCY
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                                                                                                                                            130
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                                                                                                    Conservative
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                                                                                                                                             15792 MW;
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97.7%;
                                                                                                              84.8%;
96.9%;
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                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                   Score 704; DB 2;
Pred. No. 2.2e-61;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 707; DB 2;
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                             B6C2147D227EEDDC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                             130 AA.
                                                                                                                                                                                                                                                                                                                                                     Papillomaviridae;
                                                                                                                                                                                                         DNA.
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                                                                                                                        Length
                                                                                                                                                                                                                                                                    papillomavirus
Caledonia.";
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                                                                                                    Indels
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RESULT 59
Q4TUF9_HPV
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Q919D0_HPV16
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Best Local
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01-DEC-2001, incey-
01-DEC-2001, sequence version
07-FEB-2006, entry version 1f
07-FEB-2006 (Fragment)
                                                                                                                                    Human papillomavirus typu
Viruses; dsDNA viruses, i
Alphapapillomavirus.
NCBI TaxID=10587;
                                                                                                                                                                                                                                                 19-JUL-2005,
19-JUL-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                       P9_HPV35
Q4TUF9_HPV35
Q4TUF9;
STRAIN=NW1215, NW1301, NW2760, and NW3793;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
Calleg-Amacias I.E., Villa L.L., Prado J.C., Kalantari M.,
Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn
Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,
Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-874(2002).
                                                                                       NUCLEOTIDE SEQUENCE.
STRAIN=NW1215, NW1301,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF404695; AAL01347.1; -; Genomi GO; GO:0042025; C:host cell nucleus; GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, Alphapapillomavirus. NCBI_TaxID=333760;
                                                                                                                                                                                                                                  E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q919D0_HPV16
Q919D0;
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                                                                                                                                                                                                                                                     sequence version entry version 6.
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Pred. No. 3.5e-61;
1; Mismatches 3
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RESULT Q84298 ID 4298 ID 298 ID D7 011 D7 011 D7 011 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 017 D7 01
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01-NOV-1996, integrated into U
01-NOV-1996, sequence version
07-FEB-2006, entry version 26.
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EMBL; DQ057310; AAY58341.1; -; Genomic_DNA.
EMBL; DQ057311; AAY58342.1; -; Genomic_DNA.
EMBL; DQ057312; AAY58343.1; -; Genomic_DNA.
EMBL; DQ057312; AAY58343.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0004677; F:DNA binding; IEA.
GO; GO:0006577; F:DNA binding; IEA.
SEQUENCE 149 AA; 18015 MW; 8354D5CFA293;
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type 16.";
J. Virol. 79:13630-13640(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D10597; BAA01447.1; -; Genomic_DNA.GO; GO:0042025; C:host cell nucleus; IEA.GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.
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Q84298 9PAPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE Fujinaga K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus
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PF00518; E6; 1.
NCE 149 AA; 1801
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                                                     GVCMKCLKFYSKISEYRRYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE 120
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                                                                                                                                                                                                                                                                            69.9%; Score 580; DB 2; Length 149; 71.5%; Pred. No. 4.4e-49; Live 13; Mismatches 28; Indels
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3; Mismatches 28
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01-AUG-1992,
07-FEB-2006,
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Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W
Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W
"The phylogenetic relationship and complete nucleotide sequence
human papillomavirus type 35.";
Virology 186:770-776(1992).
-i- puNCTION: Transorriptional transactivator. Binds double stran
DNA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00518; E6; 1.
Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger.
CHAIN 1 149 Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Isolate 35H;
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA virus
Alphapapillomavirus.
NCBI_TaxID=10587;
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EMBL; M74117; AAA46966.1; -; Genomic_DNA.
PIR; E40824; WGWL35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License

    -I- FUNCTION: This protein may be involved in the oncogenic potentia
    of this virus (associated with cancer of the uterine cervix).
    -I- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primer-directed sequencing of human papillomavirus Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delius H., Hofmann B.;
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sequence version 1.
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no RNA stage; Papillomaviridae;
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3; Mismatches 28;
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19D6 HPV16
PRELIMINARY; PI
Q919D6;
Q919D6;
O1-DEC-2001, integrated into Un:
O1-DEC-2001, sequence version 1:
O7-FEB-2006, entry version 16.
E6 protein (Fragment).
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Q4TUF4;
19-JUL-2005,
19-JUL-2005,
07-FEB-2006,
                                                                                                                                       MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physic:1 state of human papilloma cervical cancer isolates from Australia and New Caledonia Int. J. Cancer 97:868-874(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
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J. Virol. 79:13630-13640(2005).
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Alphapapillomavirus.
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EMBL; DQ057313; AAY58344.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Attribution-NoDerivs License
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RESULT 65
QATUG1 HPV31
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DT 19-UUL-2005;
DT 07-PEB-2006;
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July GO:0003677; F:DNA binding; IEA.
InterPro; IPR00134; E6.
Refam; PF00518; E6; 1.
SEQUENCE 103
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Best Local S
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Q1-9B2;
Q1-DEC-2001, integrated into Un
Q1-DEC-2001, sequence version 1
Q7-FEB-2006, entry version 16.
E6 protein (Fragment).
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SEQUENCE
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Viruses, dsDNA viruses, no
Alphapapillomavirus.
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InterPro; IPR00133;
Pfam; PF00518; E6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-2184229; PubMed-11857370; DOI=10.1002/ijc.10103; Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papilloma cervical cancer isolates from Australia and New Caledonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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Pred. No. 1.6e-44;
1; Mismatches 2
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VE6 HPV31
P17386;
01-AUG-1990,
01-AUG-1990,
07-FEB-2006,
Protein E6:
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STRAIN-BR1213, BR1692, and MR9917;

PubMed=16277283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16277283; DOI=10.1128/JVI.79.21.13630-13640.2005;

Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.

Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,

Chu T.Y., Cubke H.A., Cuschieri K., von Knebel-Doeberitz M.,

Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;

"Worldwide genomic diversity of the high-risk human papillomavirus
types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus typ
Viruses; dsDNA viruses,
Alphapapillomavirus.
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EMBL;
MEDLINE=89299478; PubMed=2545036; Goldsborough M.D., Disilvestre D., Temple G.F. "Nucleotide sequence of human papillomavirus neoplasia-associated virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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J. Virol. 79:13630-13640(2005).
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Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=E6;
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Name=E6;
                                                                                                                                                                                    Virology
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                                                                                        TRANSFORMATION.
MEDLINE=22188366; PubMed=12200142;
                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                          INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL; DQ057307; AAY58338.1; -; Genomic_DNA.
IL; DQ057308; AAY58339.1; -; Genomic_DNA.
III; DQ057305; AAY58339.6.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
PUENCE 149 AA; 17768 MW; 61C2A96EAC26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence version entry version 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                    type 31.
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Pred. No. 1.2e-43;
6; Mismatches 34
                                                                                                                                       AND
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                                                                                                                                     INHIBITION
                                                                                           DOI=10.1016/S0006-291X(02)02041-7;
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pe 31: a cervical
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                                                                                                                                       E6-MEDIATED
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Best Local
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JG5 HPV31
Q4TUG5 HPV31
Q4TUG5,
19-UUL-2005, i
19-UUL-2005, i
19-UUL-2005, i
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"Role of the PDZ domain-binding motif of t pathogenesis of human papillomavirus type J. Virol. 78:12366-12377(2004).
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ZN_FING
MOTIF
SEQUENCE
NUCLEOTIDE SEQUENCE.
STRALN=KK31A, KK31B, HK31C, and TL2069;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
Palbeja-Macias I.E., Villa L.L., Prado J.C., Kalantari M
Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Du
Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz
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PDZ DOMAIN-BINDING
PubMed=15507623; DO
                                                                                                                                                                                                 Human papillomavirus type
Viruses; dsDNA viruses no
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                                                                                                                                                                              Viruses; dsDNA viruses, Alphapapillomavirus.
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                                                                                                                                                                                                                                                     Name=E6;
                                                                                                                                                                                                                                                                          E6 protein.
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- SUBCELLULAR
- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-protein ligase, the human TP53/p53 tumor suppressor protein by targeting it to degradation. Binds and targets human MUPP1/MPDZ protein to degradation. Those two functions presumably contribute to transforming activity (By similarity). Interaction with human FBLN1 protein also seems to be linked to cell transformation. SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which interacts with human P53. Binds to human FBLN1 and MPDZ (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Transcriptional transactivator. Binds double stranded DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
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Yranscription; Transcription regulation; Zinc; Zinc-
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17714 :
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DOI=10.1128/JVI.78.22.12366-12377.2004;
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Pred. No. 1.
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61D2A86C362767D9 CRC64;
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/FTId=PRO_0000133351.
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                      stage; Papillomaviridae;
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                       Allan B.,
S.T.,
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Best Local
Matches 9
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HPV33
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P06427;
01-JAN-1988,
01-JAN-1988,
07-FEB-2006,
                                                                                                                                                                                                                                                         "Genome organization and nucleotide sequence of human papillomavirus type 33, which is associated with cervical cancer.";
J. Virol. 58:991-995 (1986).
-!- FUNCTION: Transcriptional transactivator. Binds double stranded DNA (By similarity).
-!- FUNCTION: This protein may be involved in the oncogenic potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; DQ057303; AAY58334.1; -; Genomic_DNA.
EMBL; DQ057304; AAY58335.1; -; Genomic_DNA.
EMBL; DQ057306; AAY58333.1; -; Genomic_DNA.
EMBL; DQ057302; AAY58333.1; -; Genomic_DNA.
EMBL; DQ057302; AAY58333.1; -; Genomic_DNA.
GQ; GQ:00042025; C:host cell nucleus; IEA.
GQ; GQ:0003677; F:DNA binding; IEA.
SEQUENCE 149 AA; 17714 MW; 61D2A86C362767D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type 16.";
J. Virol. 79:13630-13640(2005).
Activator; DNA-binding; Barly protein; Metal-binding; Nuclear protein; Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger. CHAIN

1 149

/FIId=PRO 0000133353.

ZN_FING 30 66 Potential.
                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=86200464; PubMed=3009902;
Cole S.T., Streeck R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 33.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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                                                                                                             EMBL; M12732; AAA46958.1; -; PIR; A03683; W6WL33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein E6
                                                                                 Pfam; PF00518; E6;
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                                                                                                                                                                                                       of this virus (cervical neoplasia-associated virus).
SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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                                                                                                IPR001334; E6.
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Pred. No. 1.9e
18; Mismatches
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.9e-43;
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RESULT 70
Q91ZG6_HPV58
ID Q91ZG6_HPV58
AC Q91ZG6;
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Q8QSET HPW
Q8QSET HPW
ID Q8QSE
D7 01-UU
D7 01-UI
D7 01-UI
D7 01-UI
D7 07-FE
D8 E6 pT
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Best Local
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QBQSE7;
QBQSE7;
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01-JUN-2002,
07-FEB-2006,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=E6/E7-HK-8;
MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan I
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58 variant with the x-
cervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type Viruses, dsDNA viruses, no Alphapapillomavirus.
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                                                                                                            KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
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149 AA; :
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pred. No. 1.7e-41;
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Pred. No. 3.
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3.7e-43;
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PRELIMINARY;

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RESULT 71
O90723 HPV67
ID O90723 H
AC O90723 T
DT 01-NOV-1
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DT 01-NOV-1
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OS Human pa
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RN (1)
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Best Local S
Matches 94
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EMBL; AP478152; AAL85397.1; -; Genomic_DNA.
EMBL; AP478153; AAL85408.1; -; Genomic_DNA.
EMBL; AP478154; AAL85399.1; -; Genomic_DNA.
EMBL; AP478154; AAL85399.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 149 AA; 17780 MW; 7CB6DCCC5D31B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000,
01-OCT-2000,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                             O90723 HPV67 PRELIMINARY; PRT; 149 AA. O90723; O1-NOV-1998, integrated into UniProtKB/TrEMBL 01-NOV-1998, sequence version 1.
NUCLEOTIDE SEQUENCE.
MEDLINE=99073695; PubMed=9857984; DOI=
Kirii Y., Matsukura T.;
"Nucleotide sequence and phylogenetic
papillomavirus type 67.";
Virus Genes 17:117-121(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chan P.K.S., Lam C.W., Ch
Cheung J.L.K., Cheng A.F.
"Association of human pap
cervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                           Alphapapillomavirus.
NCBI_TaxID=37120;
                                                                                                                                                                                                                                            Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-3, E6/E7-HK-5,
                                                                                                                                                                                                                                                                        Human papillomavirus type 67
                                                                                                                                                                                                                                                                                                                                 07-FEB-2006,
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                                                                                                                                                                                                                                                  dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer Inst. 94:1249-1253 (2002).
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no RNA
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Pred. No. 2.2e-41
0; Mismatches 3
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                                                                                                            DOI=10.1023/A:1008002905588;
                                                        classification
                                                                                                                                                                                                                                               Papillomaviridae
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19-JUL-2005,
07-FEB-2006,
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GO; GO:00
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Q4TUG8_I
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                                                                                                                                                                                                                                                                                      PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005; Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantaxi M., Allan B., Williamson A.L., Chung L.P., Collega, J., Zuna R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.; "Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10598;
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                J. Virol. 79:13630-13640(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=E6;
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                                                                                                                   Local
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GO:0042025; C:host cell nucleus; IEA.
GO:003577; F:DNA binding; IEA.
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NCE 149 AA;
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AVCKVCLRLLSKISEYRHYNYSLYGETLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLD
                                                  RKKRFHNISNRWTGRCSVCWRPQRTQTQ 148
                                                                                                                                                          149 AA;
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                                                                                                                                                          17807 MW;
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Pred. No. 5.4e-41;
2; Mismatches 37;
                                                                                                                  Score 497; DB 2;
Pred. No. 6.8e-41;
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                                                                                                        Mismatches
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151

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RESULT 73

Q91ZG5 HPV58
ID Q91ZG5 HPV58
AC Q91ZG5;
DT 01-CCT-2000, i
DT 01-CCT-2000, i
DT 01-FEB-2006, e
DE 6 protein.
OS Human papillom
OC Viruses; dsDNA
OC Alphapapillom
OX NCBL TaxID=105
RN NUCLEOTIDE SEC
RC STRAIN=E6HK3;
RA Chan P.K.S., I
RA Chan P.K.S., I
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01-AUG-1992;
07-FEB-2006;
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virology 185:424-427(1991).
-I- FUNCTION: Transcriptional transactivator.
DNA (By similarity).
                                                                                                            MEDLINE=92024102; PubMed=1656594;
Kirii Y., Iwamoto S., Matsukura T.;
"Human papillomavirus type 58 DNA s
                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type !
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 58. Viruses; dsDNA viruses, no RN Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=E6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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149 AA; 17863 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry version 28.
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                                                                                                                                                                                                                                                                                                                                                                               Papillomaviridae;
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24-MAY-2005,
07-FEB-2006,
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                           types 31, type 16.";
J. Virol.
                                                    NUCLEOTIDE SEQUENCE.

STRAIN=ED1710, ED1767, ED6197, HK2178, and OK332;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Juliamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Denna H.U.;

Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;

"Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.

STRAIN=66/E7-HK-1, E6/E7-HK-10, E6/E7-HK-11, E6/E7-HK-12, E6/E7-HK-13, STRAIN=66/E7-HK-15, E6/E7-HK-16, E6/E7-HK-2, E6/E7-HK-4, E6/E7-HK-6, E6/E7-HK-7, and E6/E7-HK-9; E6/E7-HK-7, and E6/E7-HK-9; DOI=10.1093/jnci/94.16.1249; MEDLINE=2216796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Cheng A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q547M1_HPV58
Q547M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                       "Association of human cervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                                                                                                                                                            E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Pfam; PF00518; E6; 1.
Activator; DNA-binding; Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90400; BAA31845.1; -; Genomic_DNA.
PIR; E36779; W6WL58.
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                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type
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103
149
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                                                                                                                                                                                                                                                                                                                                                                                                   RNA stage; Papillomaviridae;
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Pred. No. 8.5e-41;
Wismatches 36;
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                                                        papillomavirus
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RESULT 76
Q80HQ3 HPV
Q80HQ6 OP O1-JI
DT 01-JI
DT 01-JI
DT 01-JI
DT 01-JI
DT 01-JI
DT 07-PF
DE E6 PF
OS Human
OC Virua
OC Virua
OC NCBI
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Best Local S
Matches 93
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QBQHQ3 HPV58
QBQHQ3;
QBQHQ3;
QBUQ3;
Q1-JUN-2002, integrated into
Q1-JUN-2002, sequence version
Q7-FEB-2006, entry version 1
                                                                                                  NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

STRAIN=E6/E7-HK-17, and E6/E7-HK-18;

STRAIN==2176/96; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;

MEDDINE=22176/96; PubMed=17.189229; DOI=10.1093/jnci/94.16.1249;
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                                                        Chan P.K.S., Lam C.W., Cheung T.H., Li W.W. Cheung J.L.K., Cheng A.F.; "Association of human papillomavirus type cervical cancer.";
                                                                                                                                                                                                                                                Human papillomavirus type 58.
Viruses, dsDNA viruses, no RN
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence type 58 from Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=E6HK1;
Chan P.K.S.,
Copyrighted
                                         J. Natl. Cancer Inst. 94:1249-1253(2002).
                                                                                                                                                                                                                          NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                               protein
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GO: 0003677;
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AF478156; AAL85401.1;
AF478158; AAL85403.1;
AF478159; AAL85404.1;
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7; AAYSB328.1; -; Genomic_DNA,
8; AAYSB329.1; -; Genomic_DNA,
8; AAYSB330.1; -; Genomic_DNA,
9; AAYSB330.1; -; Genomic_DNA,
1; AAYSB330.2; -; Genomic_DNA,
1; AALBS398.1; -; Genomic_DNA,
1; AALBS398.1; -; Genomic_DNA,
1; AALBS401.1; -; Genomic_DNA,
6; AALBS401.1; -; Genomic_DNA,
6; AALBS401.1; -; Genomic_DNA,
6; AALBS401.1; -; Genomic_DNA,
1; AALBS404.1; -; Genomic_DNA,
1; AALBS409.1; -; Genomic_DNA,
2; AALBS409.1; -; Genomic_DNA,
3; AALBS409.1; -; Genomic_DNA,

  the UniProt
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Consortium, see
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                                                                                                                                                                                                                                                                        RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 496; DB 2;
Pred. No. 8.5e-41;
0; Mismatches 36
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79B3DCC95831B158 CRC64;
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Attribution-NoDerivs License
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                                                                                  83
http://www.uniprot.org/terms
                                                                                variant
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RESULT ID 887, ID 887, ID 887, ID 887, ID 987, ID 97, ID 9
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07-FEB-2006, entry version 25.
E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA
unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=HPV16; TISSUE=Cervical tissue; Haegert D.G., Galutira D.F., Younghusband B.H.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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EMBL; AF478167; AAL85412.1; -; Genomic_DN
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0042025; C:host cell nucleus GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q80887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q80887_9PAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U14516; AAB60570.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
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                                                 102
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                         RCINXQKPLCPEEKQRHLDKKQRFHNIRGRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNKRFHNISGRWTGRCAVCWRP--RRRQTQV
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                                                                                                  VYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISEYRYYCYSVYGTTLEQQYNKPLCDLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVCKVČLRLLSKISEYRHYNYSLYGETLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
RCINCOKPLCPBEKORHLDKKORFHNIRGRW
                                                                                                                                                                                                                                                                                                                                                                                                IPR001334; E6.
                                                                                                                                                                                                                                                                                             91
91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AA;
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                11136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17808 MW; 7803DD78E831B159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.8%;
                                                                                                                                                                                                                       59.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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Pred. No. 8.5e-41;
0; Mismatches 36
                                                                                                                                                                                                                       Score 495; DB 2;
Pred. No. 6.4e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                  22FDF3EA185ACBA7 CRC64;
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                                                 132
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                                                                                                                                                                                                                                            Length
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RESULT 78
Q4TUH6_HPV52
ID Q4TUH6_HPV52

PRELIMINARY;

PRT;

148

8

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RESULT 79
VE6 HPV52
ID VE6 HPV52
AC P36B14;
DT 01-JUN-1994, 1
DT 01-JUN-1994, 8
DT 07-FEB-2006, 6
     RRR COCCOCCETTION
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Best Local S
Matches 88
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19-JUL-2005,
07-FEB-2006,
                                                                                                                                 Human papillomavirus type 52.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Callaja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., Allan Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunn T., Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V., Sanchez G.I., Bosch X., Bernard H.-U.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus ty,
Viruses; dsDNA viruses,
Alphapapillomavirus.
NUCLEOTIDE SEQUENCE [GENOMIC DNA] MEDLINE=94265501; PubMed=8205838; Delius H., Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005; Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B. Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.; "Worldwide genomic diversity of the high-risk human papillomavirus."
                                                                                                                                                                                                                                            Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L; DQ057292; AAY58323.1; -; Genomic DNA.
GG:0042075; C:host cell nucleus; IEA.
GG:0003677; F:DNA binding; IEA.
UENCE 148 AA; 17913 MW; 2BE9D590611AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVEKPLSEITIRCIICQTPLCPEEKERHVN
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                                                                                                                                                                                                                                                               sequence version entry version 27
                                                                                                                                                                                                                                                                                                                      integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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o RNA stage;
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Pred. No. 2.1e-40;
19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
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                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                            Papillomaviridae;
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RESULT 80
QATUH4 HPV52
AC QATUH4]
DT 19-JUL-2005, 8
DT 19-JUL-2005, 8
DT 19-JUL-2005, 8
DT 19-JUL-2005, 8
DT 07-FEB-2006, 9
DE E6 protein.
GN Name=E6;
OS Human papillon
OC Alphapapillon
OC Alphapapillon
OC Alphapapillon
OC NCBI_TaxID=106
RN (1]
RN NUCLEOTIDE SEC
RC STRAIN=HK1243
RX Calleja-Macias
RA Calleja-Macias
RA Calleja-Macias
RA Calleja-Macias
RA Milliamson A.I
RA Chu T.Y. Cub
RA Marting C.R.,
RT type 16.";
RI type 16.";
RI J. Virol. 79:1
RN [2]
RP NUCLEOTIDE SEC
RC STRAIN=HK1243
RA Callaja-Macias
RA Williamson A.
RA Chu T.-Y. Cub
RA Sanchez G.I.,
RA Chu T.-Y. Cub
RA Submitted (MA)
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus typ
Viruses; dsDNA viruses, 1
Alphapapillomavirus.
NCBI_TaxID=10618;
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ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                      PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005; Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B. Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T., Chu T.V., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Wartins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.; "Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus types 16.";
                               STRAIN=HK1243, and HK2571;
Callaja-Macias I.E., Kalantari M., Villa L.L., Prado J.C.,
Callaja-Macias I.E., Kalantari M., Villa L.L., Zuna R.E., Dur
Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dur
Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.,
Sanchez G.I., Bosch X., Bernard H.-U.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein; Transcription; Transcription regulation; Zinc; Zinc-finger.
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Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-I- FUNCTION: Transcriptional transactivator. Binds double son DNA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=HK1243, and
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-!- SIMILARITY: Belongs to the papillomaviruses E6 p
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EMBL; DQ057295; AAY58326.1; -; Genomic_DNA.
EMBL; DQ057290; AAY58321.1; -; Genomic_DNA.
GO; GO:0042025; C:host_cell_nucleus; IEA.
GO; GO:0003677; F:DNA_binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BR0258, ED123, and ED18604; Callaja-Macias I.E., Kalantari M., Villa L.L., Prado J.C Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M. Sanchez G.I., Bosch X., Bernard H.-U.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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STRAIN-BR0258, ED123, and ED18604;

PubMed=1627283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=1627283; DOI=10.1128/JVI.79.21.13630-13640.2005;

Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,

Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,

Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,

Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;

"Worldwide genomic diversity of the high-risk human papillomavirus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 5
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Alphapapillomavirus.
NCBI_TaxID=10618;
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EMBL; DQ057293; AAY58324.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; TEA.
GO; GO:0003577; F:DNA binding; IEA.
SEQUENCE 148 AA; 17926 MW; OCE9C7D7341A
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                                                                                                           SEQUENCE
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InterPro; IPR001334; E6.
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Activator; DNA-binding; Early protein; Metal-binding; Nuclear Activator; DNA-binding; Early protein; Zinc; Zinc-finger.
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Distributed
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Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-I- FUNCTION: Transcriptional transactivator. Binds double s
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01-NOV-1996, f
01-NOV-1996, f
07-FEB-2006, f
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Q80883;
Q1-NOV-1996, integrated into U
01-NOV-1996, sequence version
07-FEB-2006, entry version 25.
                                                                                                                                                                                                                                                                                                                                         STRAIN-HPV16; TISSUE=Cervical tissue; Haegert D.G., Galutira D.F., Younghusband B.H.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                 EMBL; U14512; AAB60566.1; -; Genomic_DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA. InterPro; IPR0011314; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus.
Viruses; dsDNA viruses, no RNA
unclassified Papillomaviridae.
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Greenspan D., de Villiers E.-M.;
"Novel HPV types present in oral papillomatous
with HIV infection.";
Pfam; PI
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DOI=10.1002/(SICI)1997-0215(19960516)66:4<453::AID-IJC7>3.0.CO;2-V;
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:NNA binding; IEA.
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:NNA binding; IEA.
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Viruses; dsDNA viruses, no
Alphapapillomavirus
NCBI TaxID-45240;
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Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          EMBL; X67160; CAA47632.1; -; Genomic_DNA. InterPro; IPR001334; E6.
                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                        I Conguet M., Beaudenon S., Orth G.,
"Two novel genital human papillomavirus (HPV)
related to the potentially oncogenic HPV39.",
J. Clin. Microbiol. 34:738-744(1996).
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07-FEB-2006, entry version
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                                                                                               -!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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MEDLINE=97060129; PubMed=8904450;
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                             FUNCTION: Transcriptional transactivator. Binds
                                                                                                                                                                                                                                                 DNA (By similarity)
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o RNA stage;
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                              Score 468.5; DB 1;
Pred. No. 4.7e-38;
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Potential
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Pred. No. 4.7e-39
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Best Local S
Matches 88
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_HPV70
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01-OCT-1996,
01-OCT-1996,
07-FEB-2006,
                                                                                                                                                                 ZN_FING
ZN_FING
CONFLICT
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                  "Two novel genital human papillomavirus (HPV) types, related to the potentially oncogenic HPV39."; J. Clin. Microbiol. 34.738-744 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forslund O., Hansson B.G.;
"Human papillomavirus type 70 genome cloned products: complete nucleotide sequence and g J. Clin. Microbiol. 34:802-809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus typ
Viruses; dsDNA viruses,
Alphapapillomavirus.
MCBI_TaxID=39457;
                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                MEDLINE=97060129; PubMed=8904450;
Longuet M., Beaudenon S., Orth G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [GENOMIC DNA] MEDLINE=96249586; PubMed=8815087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                      InterPro; IPR001334; E6.
Pfam; P00518; E6; 1.
Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
Pranscription; Transcription regulation; Zinc; Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
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  122
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U22461; AAC54880.1;
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                        64
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                                                                                                                      Similarity
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                       ACOKCIKFHAKVRELRHYSNSVYATTLESITNTKLYNLSIRCMSCLKPLCPAEKLRHVNT 123
                                 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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                                                                  FPNPAERPYKLPDLCTALDTTLHDITIDCVYCKTQLQQTEVYEFAFSDLFIVYRNGEPYA
                                                                                  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
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105
100
                                                                                                              Conservative
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141
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O RNA
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MW; 6B610800D923D6DE
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                                                                                                                      Score 468.5;
Pred. No. 4.7
                                                                                                                                                                  Potential.
N -> D (in Ref.
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Genomic_DNA.
                                                                                                                                                                                                             regulation; Zinc;
Protein E6.
                                                                                                                                                                                        Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stage; Papillomaviridae;
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
                                                                                                                       4.7e-38;
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                                                                                                                                  DB 1;
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                                                                                                                                                          CRC64;
                                                                                                                                  Length 158;
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124

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RESULT
VE6_HPV
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Best Local
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IDS_HPV68
Q2VJDS_HPV68
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
                                       Lungu O., Crum C.P., Silverstein S.J.;
"Biologic properties and nucleotide sequence analysis of human
papillomavirus type 51.",
J. Virol. 65:4216-4225(1991).
-i- FUNCTION: Transcriptional transactivator. Binds double stranded
DNA (By similarity).
-i- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VE6_HPV51
P26554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 68a.
Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Plasmid 952;
PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2006, integrated III-
10-JAN-2006, sequence version
07-FEB-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, Alphapapillomavirus.
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                                                                                                                                                                                                                     MEDLINE=91303675;
                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus
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                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10595;
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virol. 79:15503-15510(2005).
                    SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
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NCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;
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                                                                                                                                                                                                                     PubMed=1649326;
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                                                                                                                                                                                                                                                                                                                                                type s
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o RNA stage;
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Pred. No. 4.
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                    papillomaviruses
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                  E6 protein
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                    family.
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Best Local S
Matches 86
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ZN FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991,
01-JUN-1994,
07-FEB-2006,
Protein E6.
VE6_HPV45
P21735;
                                                                               EMBL; X74479; CAA52573.1;
EMBL; M38198; AAA46973.1;
PIR; S36561; S36561.
                                                                                                                                                                                                                 Kaplan J.B., Burk R.D.; Submitted (AUG-1990) to the EMBL/GenBank/DDBJ-I- FUNCTION: Transcriptional transactivator.
                                                                                                                                                                                                                                                                Pelius H., Hofmann B.;
Delius H., Hofmann B.;
"Primer-directed sequencing of human papillomavirus types.";
"Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus typ
Viruses, dsDNA viruses,
Alphapapillomavirus
                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                    Name=E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001334; E6. Pfam; PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                  -!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                               -!- FUNCTION: This protein has transforming activity in vitro.-!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By simila
                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
                                                                                                                                                                                                       DNA (By similarity).
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151 AA;
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Genomic_DNA.
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Pred. No. 3.1e-37;
4; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae.
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GG:0042025; C:host cell nucleus;
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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87; Conserv
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integrated into UniProtKB/Swiss-Prot.
sequence version 1.
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R -> P (in Ref. 2).
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R -> A (in Ref. 2).
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2; Mismatches
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Pred. No. 3.3e-37;
0; Mismatches 2;
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Pred. No. 3.6
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Name=E6;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94037097; PubMed=8221889; DOI=10.1016/0092-8674(93)90384-3; Scheffner M., Huibregtse J.M., Vierstra R.D., Howley P.M.; "The HPV-16 E6 and E6-AP complex functions as a ubiquitin-protein ligase in the ubiquitination of p53."; Cell 75:495-505(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=87053870; PubMed=3023067;
Schneider-Gaedicke A., Schwarz E.;
"Different human cervical carcinoma cell lines "Different human cervical carcinoma cell lines "transcription patterns of human papillomavirus "Transcription patterns of human papillomavirus"
MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7; Du M., Fan X., Hong E., Chen J.J.; "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1."
                                                                                                                                                                                               DOI=10.1128/JVI.74.20.9680-9693.2009,
Lee S.S., Glaunsinger B., Mantovani F., Banks L., Jav
"Multi-PDZ domain protein MUPPI is a cellular target
adenovirus E4-ORF1 and high-risk papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grossman S.R., Laimins L.A.; "E6 protein of human papillomavirus Oncogene 4:1089-1093(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINB=87218459; PubMed=3034571;
Seedorf K., Olteredorf T., Kraemer G., Roewekamp W.;
Seedorf K., Olteredorf T., Kraemer G the human papilloma viruses
"Identification of early proteins of the human papilloma viruses
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
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MEDLINE=88188247; PubMed=2833614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matlashewski G., Banks L., Wu-Liao J., Spence "The expression of human papillomavirus type I and the production of anti-E6 antibodies."; J. Gen. Virol. 67:1909-1916(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses repeated structure of the E6 and E7 gene products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=87283882; PubMed=3039146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH HUMAN TP53 PROTEIN. MEDLINE=94037097; PubMed=8221889; DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T.,
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                                                                            TRANSFORMATION
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                                                                                                                                                                                                                                                                                                         MEDLINE=20457232; PubMed=11000240
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                                                                                                   INTERACTION WITH HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5:2285-2292(1986).
                                                                                                                                                     74:9680-9693 (2000)
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rget for both
type 18 E6
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RESULT Q76291 ID Q76291 AC Q7 AC Q7 AC Q7 DT 100 DT 100 DT 07 DE E6 GN Na GN Hu OCC V11 CC V1 CC
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Best Local
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10-MAY-2005,
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SEQUENCE
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                                      Human papillomavirus type 18.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333761;
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EMBL; X05015; CAA2864.1; -; Genomic_DNA.
EMBL; M20325; AA39514.1; -; GRING.
EMBL; M26798; AAA46946.1; -; Genomic_DNA.
EMBL; X04773; CAA28466.1; -; Genomic_DNA.
EMBL; X04374; CAA00539.1; -; Unassigned_DNA.
EMBL; A06324; CAA00542.1; -; Unassigned_RPSL; A06328; CAA00542.1; -; Unassigned_RPSL; A06328; CAA00542.1; -; Unassigned_RPSL; A06328; CAA00542.1; -; Unassigned_RPSL; A26165; W6WL18.
                                                                                                                                                                   E6 protein.
                                                                                                                                                                                                                                                                     Q76Z97
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  NUCLEOTIDE SEQUENCE
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Activator; DNA-binding; Early
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SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which interacts with human P53. Binds to human PBLN1 and MPDZ.
SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the papillomaviruses E6 protein family
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FUNCTION: Transcriptional transactivator. Binds double strans DNA (By similarity). Has transforming activity. Inactivates, E6-AP ubiquitin-protein ligase, the human TP53/p53 tumor suppressor protein by targeting it to degradation. Binds and targets human MUPPI/MPDZ protein to degradation. Those two functions presumably contribute to transforming activity.
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                                                                                                                                                                                             integrated into UniProtKB/TrEMBI sequence version 1. entry version 4.
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18872 MW;
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                                                                                              RNA stage; Papillomaviridae;
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Pred. No. 9e-37;
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TQV->DQA: Complete loss of binding
MPDZ protein.
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/FTId=PRO_0000133338.
Potential.
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Best Local
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01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
            ZN_FING
                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae. NCBI_TaxID=10602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Papillomaviruses.";
J. Virol. 79:15503-15510(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0042025;
GO; GO:0003677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity-
-!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                                                                                                        grainoma cell line ME180.";
J. Virol. 65:5564-5568(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00518;
SEQUENCE 158
SEQUENCE
                                                              Activator; DNA-binding; Early protein; Metal-binding; Nuclear Transcription; Transcription regulation; Zinc; Zinc-finger.
                                                                                           InterPro; IPR001334; E6. Pfam; PF00518; E6; 1.
                                                                                                                   EMBL; M73258; -; NOT_ANNOTATED_CDS; PIR; C40509; W6WLPR.
                                                                                                                                                                                                                                                                                   Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen "Characterization of a novel human papillomavirus DNA
                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC MEDLINE=91374616; PubMed=1716
                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type ME180
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY262282; AAP20594.1; -; Genomic
GO; GO:0042025; C:host cell nucleus; IE
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narechania A., Chen Z., Desalle E
"Phylogenetic Incongruence among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
                                                                                                                                                                                                                                              -!- FUNCTION: Transcriptional transactivator. Binds double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPVME
                                                                                                                                                                                                                               DNA (By similarity)
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQDPQERPKKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRRFHNIAGHYRGOCHSCCNRAROERLORRRETOV
158 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence version entry version 28.
                         32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E6; 1.
AA; 18872 MW;
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Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                              CE [GENOMIC DNA].
PubMed=1716694;
                                                   158
                           68
18739
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Μ¥.
                                                                                                                                                                                                                                                                                                                                                                                  RNA
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Pred. No. 9e
              Potentia
                        Potential
                                   Protein E6.
/FTId=PRO_0000133318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                  stage;
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2B1F406B563F05FC CRC64
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                                                                                                                                Genomic_DNA.
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mavirus DNA in the cervical
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Length 158;

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RESULT 96
Q7KYK8 HPV68
ID Q7KYK8 HPV68
ID Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KYK8 TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY TAC Q7KY
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Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98090464; PubMed=9427755; DOI=10.1093/emboj/17.1.215; Reuter S., Bartelmann M., Vogt M., Geisen C., Napierski I., Kahn T., Delius H., Lichter P., Weitz S., Korn B., Schwarz E.; Delius H., Lichter P., Weitz S., Korn B., Schwarz E.; Papm-1, a novel human gene, identified by aberrant cotranscription with papillomavirus oncogenes in aa cervical carcinoma cell line, encodes a BTB/POZ-zinc finger protein with growth inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=91374616; PubMed=1716694;
MEDLINE=91374616; PubMed=1716694;
Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen
"Characterization of a novel human papillomavirus DNA
carcinoma cell line ME180.";
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004,
05-JUL-2004,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SL; Y14591; CAA74931.1; -; mRNA.
GO:0042025; C:host cell nucleus;
GO:0003677; F:NNA binding; IEA.
erPro; IPR001334; E6.
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123
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86; Conserv
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                                                    KKQRFHNIRGRWTGRCMSCCRSS-----RTRRETQL 151
                                                                                                                                                                                                                                                       MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKQRFHNIRGRWTGRCMSCCRSS-----RTRRETQL
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                                                                                                                                                                                                                      LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
SKRRFHKIAGNFTGQCRHCWTSKREDRRRTRQETQV
                                                                                                                                             AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                            AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   18739 MW;
                                                                                                                                                                                                                                                                                                                                54.4%; Score 451.5; DB 2;
55.1%; Pred. No. 2.2e-36;
tive 21; Mismatches 44;

    k; Score 451.5; DB 1;
    k; Pred. No. 2.2e-36;
    21; Mismatches 44;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  see http://www.uniprot.org/terms
Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                              158;
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RESULT 97
QSUIZ9_9PAPI
ID QSUIZ9_9PAPI
AC QSUIZ9_9PAPI
AC QSUIZ9_1
DT 01-MAY-2000, |
DT 07-FEB-2006, |
DE E6.
OX NCBI_TAXID=100
CN NCBI_TAXID=100
RN NUCLEOTIDE SER
RN MEDLINE=91374
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VE6_HPV39
P24835;
                                                          type 39.";
Virology 181:419-423(1991).
-!- FUNCTION: Transcription
DNA (By similarity).
                                                                                                                                                                                                                                                                                    Human papillomavirus tyr
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI TaxID=10588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.; "Characterization of a novel human papillomavirus DNA in the cervical carcinoma cell line ME180.", J. Virol. 65:5564-5568(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified Papi
NCBI_TaxID=10566;
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07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses, dsDNA viruses, no RNA unclassified Papillomaviridae.
                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=91135017; Pubmed=1847266;
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91374616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus.
                                                                                                                                                                                             Volpers C., Streeck R.E.
                                                                                                                                                                      "Genome organization
FUNCTION: This protein may be involved in the oncogenic of this virus (cervical neoplasia-associated virus). SUBCELLULAR LOCATION: Nuclear matrix-associated (By simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L; M73258; AAF14011.1; -; Genomic DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
erro; IER001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00518; E6; 1.
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llarity 55.1%;
Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19167 MW;
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7 RNA
                                                                                                                                                                           nucleotide
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Pred. No. 2.3e-36;
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                                              Query Match
Best Local S
Matches 86
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Best Local
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Pfam; PFOC
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01-MAY-2000, integrated into 1
01-MAY-2000, sequence version
07-FEB-2006, entry version 17
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ZN FING
SEQUENCE
                                                                                                                                                                                                        EMBL; Y18491; CAB53096.1; -; Genomic_DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of E6 and E7 Genes of Transformation Potential of E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activator; DNA-binding; Early protein; Metal-binding; Nuclear Oncogene; Transcription; Transcription regulation; Zinc; Zinc CHAIN 1 158 Protein E6.
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Veiko V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
Laassri M., Gul'ko L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIAGH BAND6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M62849; AAA47050.1; -; Genomic_DNA.
PIR; A38502; W6WL39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kisseljev F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=333761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001334; E6. Pfam; PF00518; E6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                        PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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                                              66;
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                                                                      Similarity
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  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRRFHKIAGSYTGOCRRCWTTKREDRRLTRRETOV 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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                                                                                                                                                                                    IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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105
158 AA;
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                                              Conservative
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                                                                                                                       11.
18886 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vinokurova
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                                              21;
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                                         Score 449.5; DB 2;
Pred. No. 3.5e-36;
1; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 449.5;
Pred. No. 3.
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Gene a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papilloma Virus Type 18 and and its Mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kisseljova N., Veiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papillomaviridae,
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Terai M., Burk R.D.;
Terai M., Burk R.D.;
"Cervical HPVs in Evolution; Genomic Sequence of IS39/AB2,
of Oncogenic HPV 82 (W13B).";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF293961; AAK28449.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA. InterPro; IPR001334; E6.
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PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses,
Alphapapillomavirus.
MCBI_TaxID=129724;
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01-JUN-2001, sequence version
07-FEB-2006, entry version 17
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J. Virol. 79:15503-15510(2005).
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RESULT 1
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; Sequence 5, Application US/10530253
; Publication No. US20060014926A1
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
                                          US-10-530-253-5
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SEQ ID NO 3
LENGTH: 248
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                           SEQ ID NO 5
                                                                                                                                           APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
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NUMBER OF SEQ ID NOS: 65
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry
                                                       TYPE: PRT ORGANISM: Human papillomavirus type 16
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                                                                                                          LENGTH:
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No. US20060014926A1
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Pred. No. 6.5e-81;
    Score 828;
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US-10-484-063-27

(Sequence 27, Application US/10484063)

Publication No. US20050048467A1

GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORTOLERO-LUNA, GUILLERMO

APPLICANT: FOLLEN, MICHELE

TITLE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: PCT/US02/23198

PRIOR FILING DATE: 2002-07-19
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SEQ ID NO 20
LENGTH: 151
TYPE: PRT
ORGANISM: Human papillomavirus
US-10-484-063-20
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Best Local Similarity
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APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
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RESULT 5
US-10-530-253-13
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                                   RESULT 6
US-10-530-253-1
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Sequence 1, Application US/10530253 Publication No. US20060014926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Somith, Larry
APPLICANT: Somith, Larry
APPLICANT: Somith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
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PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
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TYPE: PRT
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TYPE: PRT
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                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2
                                                                                                                                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHOPPIN, APPLICANT: BOURGAUL'
APPLICANT: GUILLET,
APPLICANT: CONNAN, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 2, Application US/10858384
Publication No. US2005003300581
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Best Local
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APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
PILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US-60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
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nes 149; Conservative
                                                                                                                                                   Local Similarity
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                                                                       MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 67
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GUILLET, JEAN-GERARD
CONNAN, FRANCINE
                                                                                                                                   Conservative
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                                                                                                                            Score 823; DB 5;
Pred. No. 1.3e-80;
1; Mismatches 2
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Pred. No. 1.1e-80;
0; Mismatches 2;
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                                                                                                                                                                        Length 158;
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APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Coi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 198
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
LENGTH: 158
TYPE: PAT
CORGANISM: Homo sapiens
US-10-367-057-16
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US-11-021-949-13
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US-10-367-057-16
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US-11-021-949-13
                                                                  TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/10367057 Publication No. US20050100554A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICANT: LU, PETER
APPLICANT: GARMAN, JC
APPLICANT: BELMARES,
APPLICANT: DIAZ-SARM
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/11021949 Publication No. US20050142541A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cuthill, Scott; APPLICANT: Jackson, Amand
                                                                                                                                                                                                                                                                      APPLICANT:
            TYPE: PRT ORGANISM: human papilloma virus (HPV)
                                                      ENGTH: 158
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DIAZ-SARMIENTO, CHAMORRO SOMOZA
                                                                                                                                                                                                                                                                    SCHWEIZER, JOHANNES
                                                                                                                                                                                                                                                                                                                           GARMAN, JONATHAN DAVID
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Pred. No. 1.3e-80;
Pred. Mo. 1.3e-80;
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Sequence 2, Application US/10472724

Publication No. US20040171806A1

GENERAL INFORMATION:

APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Harald

ITILE OF INVENTION: Modified HPV E6 and E7 ge.

FILE REFERENCE: 4121-L54

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: ECT/EF02/03271

PRIOR APPLICATION NUMBER: EP 01107271.7

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: EP 01107271.7

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 27
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; Publication No. US20060039919A1
; GENERAL INFORMATION;
; APPLICANT: HealthBanks Biotech CO. LTD.
TITLE OF INVENTION: Fusion protein for inhib
; FILE REFERENCE: P7819/0613
; CURRENT APPLICATION NUMBER: US/11/206,138
; CURRENT FILLING DATE: 2005-08-18
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US-11-206-138-3
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SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 158
TYPE
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Best Local Similarity
Matches 148; Conserv
               SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 171
TYPE: PRT
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     128
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Pred. No. 1.3e-80;
l; Mismatches 2
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Pred. No. 1.3e-80;
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RESULT 13
US-10-530-253-11
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TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-530-253-9
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US-10-530-253-9
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APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                         GENERAL INFORMATION:
                                                                                                                          Sequence 11, Application US/10530253 Publication No. US20060014926A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
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98.0%; Pred. No. 1.5e-80;
tive '1; Mismatches 2
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Pred. No. 2.2e-80;
0; Mismatches 2
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US-11-192-923A-2
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US-10-530-253-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/11192923A
Publication No. US20060018928A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PANG, XIAOWU
TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
TITLE OF INVENTION: RECOMBINANT REPLICON
FILE REFERENCE: 116620-003
GURRENT APPLICATION NUMBER: US/11/192,923A
CURRENT APPLICATION NUMBER: CN 03115272.4
PRIOR APPLICATION NUMBER: CN 03115273.2
PRIOR APPLICATION NUMBER: CN 03115273.2
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SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 248
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                                                                                                                                                                                                                                              Matches
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Best Local Similarity 98.0%;
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 3.3
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                         LENGTH: 256
TYPE: PRT
ORGANISM: Human papillomavirus
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226
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                                                                                                          61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 256
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Pred. No. 2.3e-80;
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Pred. No. 2.2e-80;
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
TYPE: PAT
ORGANISM: Homo sapien
US-10-000-903-4
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Publication No. US20020081329A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT APPLICATION NUMBER: PCT/AU98/00080
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR APPLICATION NUMBER: DS/05/3198/00080
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LENGTH: 266
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                                                                                                 Query Match
Best Local (
                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fer
APPLICANT: Delisse, Anne-Marie Ghr
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human papillomavirus type 16
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                                                                                                   Similarity
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MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 173
                         MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                 2001-10-01
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                                                                                              99.2%;
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                                                                           Score 823; DB 4; I pred. No. 2.5e-80; 1; Mismatches 2;
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Pred. No. 2.4e-80;
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PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
                                                                                                                                                                                                                                                             Sequence 10, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10899771 publication No. US20050031638A1
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CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
                                                                                                               APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dalemans, Wilfried L.J. APPLICANT: Gerard, Catherine Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y Match 99.2%; Local Similarity 98.0%;
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Pred. No. 2.5e-80;
Wismatches 2;
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US-10-899-771-10
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; ORGANISM: Homo sapien
US-10-000-903-10
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REPERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR APPLICATION NUMBER: BCT/EP98/08563
PRIOR APPLICATION NUMBER: BCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-24
NUMBER: OF SEQ ID NOS: 28
NUMBER: DESERVED FOR WINDER: BCT/EP98/08563
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE PT
TYPE PT
ORGANIEM: Artificial Sequence
PEATURE:
253
                                     121
                                                                               193
                                                                                                                                                        133 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                        Similarity
                    KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                  AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFESKQRHLD
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                           AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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Pred. No. 2.7e-80;
1; Mismatches 2
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Pred. No. 2.7e-80;
1; Mismatches 2
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papil
TITLE OF INVENTION: Compositions Comprising Human Papil
TITLE OF INVENTION: and Fusion Proteins Adjuvanted wit
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/08563
PRIOR APPLICATION NUMBER: US/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6
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US-10-899-771-6
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US-10-899-771-6
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                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
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Publication No. US20020182221A1
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SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
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CURRENT FILLING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: CT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dalemans, Wilfried L.J. APPLICANT: Gerard, Catherine Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Vaccine FILE REFERENCE: 845107
                                                                                                                                               LENGTH: 37
TYPE: PRT
                  OTHER INFORMATION: Chimaeric protein (protein D
OTHER INFORMATION: influenzae B and E6E7 fusion
OTHER INFORMATION: virus type 16)
                                                                                             FEATURE:
                                                                                                                     ORGANISM: Artificial Sequence
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Pred. No. 3.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Papilloma Virus Proteins
juvanted with a CpG Oligonucleotide
                                              from Haemophilius from Human papill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 371;
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                                              papilloma
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US-10-899-771-14
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US-10-000-903-14
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                                                                                                                                                                                                            RESULT 23
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CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                      Sequence 14, Application US/10899771 Publication No. US20050031638A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 148; Conserv
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LENGTH: 390
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Best Local
            APPLICANT: Dalemans, wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                  253
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                                                                                                                                                                                                                                                                                                                                    AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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Pred. No. 3.6e-80;
1; Mismatches 2
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; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-530-253-7
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Publication No. US20060014926A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Sefirey K. Pullen
APPLICANT: Susan P. McElhiney
ITILE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
SOFTMARE: Patentin version 3.1
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PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                             Local Similarity
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KQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                    VCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDK
                                                                                                                                                    FQDPQERPRKLPQLCTELQTTIHDIILECYYCKQQLLRREYYDFAFRDLCIYYRDGNPYA 158
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98.0%;
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Pred. No. 3.7e-80;
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Pred. No. 3.8e-80;
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219

KQRFHNIRGRWTGRCMSCCRSSRTRRETQL 248

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RESULT 26
US-11-072-288-1
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; ORGANISM: Human papillomavirus type
US-10-177-390-6
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US-10-177-390-6
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/072,288
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US/09/462,993
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PR/09152
PRIOR FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PS/09152
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11072288
Publication No. US20050159386A1
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine
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APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION INWEBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10177390 Publication No. US20030143743A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 243
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Best Local
Query Match
Best Local Similarity
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APPLICANT: BIZOUARNE, Naddine
TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
FILE REFERENCE: 017753-122
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.2
                                                                                       OTHER INFORMATION: Description of Artificial Sequence:Derivated from OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein OTHER INFORMATION: fused F protein signals, clone E6*TMF.
                                                                                                                                                                       FEATURE:
                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 151
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93.9%;
94.7%;
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Pred. No. 3.4e-80;
0; Mismatches 3
Score 779.5; DB 6; Pred. No. 1.1e-75;
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GENERAL INFORMATION:

APPLICANT: LU, PETER

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: SCHWEIZER, JOHANNES

TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV

TITLE OF INVENTION: AND METHODS OF THEIR USE

FILE REFERENCE: VITA-012

CURRENT APPLICATION NUMBER: US/11/021,949

CURRENT APPLICATION NUMBER: 60/532,373
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US-10-530-253-18
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Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Jusan P. McElhiney
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
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Best Local Similarity
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71.5%;
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Pred. No. 3.6e-54;
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; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FASTSEQ for Windows Version 4.
; SEQ ID NO 14
; SEQ ID NO 14
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-14
RESULT 30

US-11-021-949-18

; Sequence 18, Application US/11021949

; Publication No. US20050142541A1

; GENERAL INFORMATION:
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US-10-530-253-16
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Matches
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: DCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
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TYPE: PRT
ORGANISM: Human papillomavirus type
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                                                                                                                                                                                                                                                                                                                                                                  63.0%; Score 523; DB 5; Length 149;
64.9%; Pred. No. 3.2e-48;
tive 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 578; DB 6; 71.5%; Pred. No. 3.6e-54; tive 13; Mismatches 28
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; SEQ ID NO 18
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-18
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                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Human papillomavirus type US-10-530-253-17
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US-10-530-253-17
VS-10-530-253-17
Sequence 17, Application US/10530253
Publication No. US20060014926A1
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                                                                                                                                                                                Query Match 62.7%; Score 520; DB 5; Best Local Similarity 63.6%; Pred. No. 6.7e-48; Matches 96; Conservative 19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 17
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Best Local Similarity
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Somith, Larry
APPLICANT: Somith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US/60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
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                                                                                                                                                                                                                                                                                                                                            LENGTH: 149
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61
                       98;
                                                                                                                     1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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GICKLCLRPLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                        MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 523; DB 6; 64.9%; Pred. No. 3.2e-48;
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; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-16
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                          SEQ ID NO 360
LENGTH: 149
TYPE: PRT
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
FITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
                                                                                                                                                                                                                                                                                                                                            APPLICANT: LU, PETER APPLICANT: GARMAN, CAPPLICANT: BELMARES,
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                         PRIOR APPLICATION NUMBER: 60/532,373
PRIOR PILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PastSEQ for Windows Version 4.0
ORGANISM: human papilloma virus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LNKRFHNISGRWAGRCAACWRS--RRRETAL 149
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                                                                                                                                                                                                                                                                                                                    DIAZ-SARMIENTO,
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o. US20050142541A1
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           GENERAL INFORMATION:

APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, JOHANNES
APPLICANT: CIMEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012

FILE REFERENCE: VITA-012
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PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
                                                                                                                                                                                                                   Sequence 15, Application US/11021949 Publication No. US20050142541A1
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Publication No. US20060014926A1
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Best Local Similarity
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
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TYPE: PRT
CURRENT APPLICATION NUMBER: US/11/021,949
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                                                                                                                                                                                                                                                                                                                                                         121 LNKRFHNÍSGRWTGRCAVCWRP--RRRQTQV 149
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Pred. No. 2.6e-45;
on. Mismatches 36;
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Pred. No. 1.6e-45;
22; Mismatches 37;
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 149
TYPE: PRT
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
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; ORGANISM: Human papillomavirus type 52
US-10-530-253-22
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                                         RESULT 37
US-11-021-949-17
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PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Seffrey K. Pullen
APPLICANT: Susan P. McElhiney
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
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US-11-021-949-359
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APPLICANT: LU, PETER;
APPLICANT: GARMAN, JC
APPLICANT: BELMARES,
APPLICANT: DIAZ-SARMI
                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 361
SOFTMARE: FastSEQ for Windows Version
SEQ ID NO 359
LENGTH: 148
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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Publication No. US20050142541A1
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
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APPLICANT: GAI
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILLING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANIDOLIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
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TYPE: PRT
ORGANISM: human papilloma virus (HPV)
                                                                                                                                          Local Similarity
es 87; Conserv
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                                                                             FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
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BELMARES, MICHAEL P.
DIAZ-SARMIENTO, CHAMORRO SOMOZA
VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                  FPNPEBRPYKLPALCEEVNISIHEIELDCVYCEROLYRCEVYDFIFRDLCVVYRKGKPLG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARMAN,
                                                                                                                                          58.3%; Score 484; DB 6; Length 148; llarity 60.4%; Pred. No. 5.le-44; Conservative 17; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.7%; Score 487; DB 6; Length 148; 61.7%; Pred. No. 2.4e-44; Live 19; Mismatches 35; Indels
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                                                                  SEQ ID NO 26
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                             APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE ONGSO/LOGALILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/LOGALIP-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PC/US2003/031726
PRIOR PETING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: WS/0/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                     NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
                       TYPE: PRT
ORGANISM: Human papillomavirus type 68
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No. US20050142541A1
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Pred. No. 6.6e-44;
.6; Mismatches 40; Indels
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US-10-530-253-21
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Sequence 21, Application US/10530253
Publication No. US20060014926A1
ENDERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Publen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 361 LENGTH: 158
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Publication No. US20050142541A1
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
ATAZ-SARMIENTO, CHAMORRO SOMOZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
RUMBER OF SEQ ID NOS: 361
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC .
TITLE OF INVENTION: AND METHODS OF THEIR USE
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                 KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
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Pred. No. 2.6e-42;
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR RILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 151
TYPE: PRT
ORGANISM: Human papillomavirus type 51
US-10-530-253-21
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-24
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Best Local Similarity 57.0
86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV TITLE OF INVENTION: AND METHODS OF THEIR USE FILE REFERENCE; VITA-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
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121
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                                   121 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                    MFEDKRERPRTLHELCEALNVSMHNIQVVCVYCKKELCRADVYNVAFTEIKIVYRDNNPY
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EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
                                                                                    AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEEKQKLVD
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DIAZ-SARMIENTO, CHAM
SCHWEIZER, JOHANNES
                                                                                                                                                                                                                                                       55.4%; Score 460; DB 6; Length 151; 57.0%; Pred. No. 2.1e-41; tive 24; Mismatches 41; Indels
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RESULT 44

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; SEQ ID NO 29
LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-29
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US-11-021-949-29
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APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LU, PETER
APPLICANT: GARMAN, JC
APPLICANT: BELMARES,
APPLICANT: DIAZ-SARM
APPLICANT: SCHWEIZER,
                                                                               Matches
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GÁRMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jeffréy K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: CT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
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les 87; Conserv
                                                                             Local Similarity es 87; Conserv
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                     FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA 63
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ilarity 56.1%;
Conservative 2
                                                                             55.4%;
llarity 56.1%;
Conservative 2
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                                                                               22;
                                                                                                  Score 459.5; DB 6
Pred. No. 2.5e-41;
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Pred. No. 2.5e-41;
                                                                                 Mismatches
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                                                                                                                     Length 158;
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      63
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APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRATILLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 158
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US-10-530-253-15
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SEQ ID NO 15
LENGTH: 158
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Best Local Similarity
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Publication No. US20060014926A1
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Someth, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US/03/031726
PRIOR APPLICATION NUMBER: US/03/03/031726
PRIOR FILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
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; Pred. No. 6.6e-41;
21; Mismatches 42;
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; TYPE: PRT ; ORGANISM: human papilloma virus (HPV) US-11-021-949-28
WS-10-00-903-21

// Sequence 21, Application US/10000903

// Publication No. US20020182221A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOPTWARE: PatentIn version 3.2
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 87; Conserv
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CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                            Local
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87; Conserv
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                                                                                                                                                                KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                       FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                           KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
                                                                                                                                                                                                                                                                                                                                                                      54.9%; Score 455.5; DB 4; llarity 56.1%; Pred. No. 7.3e-41; Conservative 21; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes and proteins useful for vaccination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 172;
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GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

REFERENCE:

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APPLICANT: Gerard, Catherine Marie Ghislaine
FITTLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FITTLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1909-12-18
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 278
TYPE: PRT
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; LENGTH: 278
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Homo Bapien
US-10-000-903-21
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US-10-899-771-21
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Best Local (
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                                                                                                                                                      Matches
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Best Local :
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dalemans, Wilfried L.J. APPLICANT: Gerard, Catherine Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                           OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus OTHER INFORMATION: 18)
                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
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FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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                                                                                       FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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56.1%; Pred. No. 1.36
tive 21; Mismatches
                                                                                                                                                    54.9%; Score 455.5; DB 5; 56.1%; Pred. No. 1.3e-40; tive 21; Mismatches 42;
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Sequence 23, Application US/10899771

Publication No. US20050031638A1

GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
ITILE OF INVENTION: Compositions Comprising Human Papilloma Virus Prot
ITILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonu
FILE REFERENCE: B45124

FILE REFERENCE: B45124

CURRENT FILING DATE: 2004-07-27

CURRENT FILING DATE: 2004-07-27

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR APPLICATION NUMBER: PGT/EP98/08563

PRIOR APPLICATION NUMBER: GB 9727262.9

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
Thes 87; Conservi
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US-10-000-903-23
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SEQ ID NO 23
LENGTH: 383
TYPE: PRT
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APPLICANT: Cabezor
APPLICANT: Delisse
APPLICANT: Gerard
APPLICANT: Lombar
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
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Publication No. US20020182221A1
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP99/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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                     383
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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Pred. No. 1.8e-40;
11; Mismatches 42
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US-11-021-949-31
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US-10-899-771-23
                                                                                                        US-10-800-023-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: human papilloma virus (HPV)
US-11-021-949-31
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                                                                                                                                    RESULT 54
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Matches
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                                           GENERAL INFORMATION
                                                               Sequence 27, Application US/10800023 Publication No. US20040258688A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 31
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARRS, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOPTMARE: FASTSEQ for Windows Version 4.0
APPLICANT: Steinman, Ralph APPLICANT: Nussenzweig, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                               127 SKRRFHKIAGNFTGQCRHCWTSKREDRRRTRQETQV 162
                                                                                                                                                                                                                                        121 KKORFHNIRGRWTGRCMSCCRSS-----RTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 54.4%; Score 451.5; DB 6; Similarity 55.1%; Pred. No. 1.8e-40; 86; Conservative 21; Mismatches 44;
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                                                                                                                                                                                                                                                                                      AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
                                                                                                                                                                                                                                                                                                                                                                        FHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
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nilarity 56.1%;
Conservative 2
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; Pred. No. 1.8e-40;
21; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 162;
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FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 158
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APPLICANT: Bonifaz, Laura
ITITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
ITITLE OF INVENTION: of the Immune Response Therefrom
FILE REFERENCE: 600-1-081CONCIPI
CURRENT APPLICATION UNMBER: US/10/800,023
CURRENT FILING DATE: 2004-03-14
PRIOR APPLICATION NUMBER: 09/925,284
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/986,704
PRIOR APPLICATION NUMBER: 09/586,704
PRIOR FILING DATE: 2000-06-05
PRIOR PILING DATE: 2000-06-05
PRIOR FILING DATE: 1996-01-31
PRIOR APPLICATION NUMBER: 09/586,701883
PRIOR FILING DATE: 1996-01-31
PRIOR APPLICATION NUMBER: 09/586,701883
PRIOR PILING DATE: 1996-01-31
PRIOR APPLICATION NUMBER: 09/3181,528
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 27
                                                                                     Matches
                                                                                                              Best Local
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APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human
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                                                                                                              Similarity
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  FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
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                                                                                                          54.2%;
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                                                                                   Score 449.5; DB
Pred. No. 3e-40;
9; Mismatches
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; SEQ ID NO 30
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-30
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                                   CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/11021949 Publication No. US20050142541A1
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Best Local S
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                                                                                                                                                                                      APPLICANT: BELMARES MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                               APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
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PRIOR PILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOPTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
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APPLICANT: SCHWEITZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
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TYPE: PRI
                    LENGTH: 151
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Similarity 55.5%;
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Pred. No. 3e-40;
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US-11-021-949-25
                                                                                                                                                               US-10-530-253-23
                                                                                                                                                                                RESULT 59
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                                                                                                        Sequence 23, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-33
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
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APPLICANT: GARN
APPLICANT: BELN
APPLICANT: DIA;
APPLICANT: SCHI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES
FILE REFERENCE: 00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: VITA-012
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TYPE: PRT
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es 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 436.5; DB b;
Pred. No. 7.1e-39;
Migmatches 43;
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Pred. No. 3.2e-40;
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                        AND IMMUNOGENIC COMPOSITIONS
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US-11-021-949-22
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US-10-530-253-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/11021949 Publication No. US20050142541A1
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LENGTH: 155
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Local Similarity 56.4%;
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                                                                                                                                                                                                                                          84;
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84; Conservative
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  KRRFHLIAHGWTGSCLGCWRQTSREPRES
                                      KORFHNIRGRWTGRCMSCCR-SSRTRRET 149
                                                                               VCRVCLLFYSKVRKYRYYDYSVYGATLESITKKQLCDLLIRCYRCQSPLTPEEKQLHCDR
                                                                                                                                                              FNNPQERPRSLHHLSEVLEIPLIDLRLSCVYCKKELTRAEVYNFACTELKLVYRDDFPYA
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; Pred. No. 8.8e-38;
17; Mismatches 47;
                                                                                                                                                                                                                                                                Score 426.5; DB 6; Pred. No. 8.8e-38;
                                                                                                                                                                                                                                             Mismatches
153
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; LOCATION: (1)..(152)
; OTHER INFORMATION: where Xaa is any amino
US-10-530-253-39
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SEQ ID NO 25
LENGTH: 160
TYPE: PRT
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 152
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Publication No. US20060014926A1
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                          Query Match
  Best Local Similarity
                                                                     ORGANISM: Human papillomavirus type 59-10-530-253-25
                                                                                                                                                                                                  APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: WS 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
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APPLICANT: Smith, Larry
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50.1%;
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Pred. No. 3.4e-37;
Score 415.5; DB 5; Pred. No. 1.4e-36;
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Gaps

0

Length 151; Indels

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GENERAL INFORMATION:

APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
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TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-32
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APPLICANT: LU, PETER
APPLICANT: GARMAN,
APPLICANT: BELMARES
                                                                                                                                                                                                                                                       Sequence 26, Application US/11021949
Publication No. US20050142541A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local (
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: U$/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                    124
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77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KORFHNIRGRWTGRCMSC-CRSSRTRRETO 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEDPTQRPYKLPDLSTTLNIPLHDIRINCVFCKGELQEREVFEFAFNDLFIVYRDCTPYA 63
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vo. US20050142541A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.1%; Score 415.5; DB 6; Length 160; 51.3%; Pred. No. 1.4e-36; tive 25; Mismatches 47; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Mismatches
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    RESULT 66
US-11-021-949-21
; Sequence 21, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STR.
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR PILING DATE: 2004-12-23
PRIOR PILING DATE: 2004-12-23
PRIOR PILING DATE: 2003-12-23
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US-11-021-949-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 20
LENGTH: 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/11021949 Publication No. US20050142541A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LU, PETER APPLICANT: GARMAN, CAPPLICANT: BELMARES,
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                                                                                                                                                                                            KORFHNIRGRWTGRCMSCCRSSRTRRET 149
                                                                                                                                                                                                                                                                            VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                             FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                                       KKRFHRISRTWTGLCLQCWRHT-TSTET
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                                                                                                                                                                                                                                                                                                                                                                                                                         46.4%; Score 385.5; DB 6
50.0%; Pred. No. 2.3e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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STRAINS OF HPV

151

DB 6;

47;

Indels Length 153;

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Gaps

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GENERAL INFORMATION:

APPLICANT: LU, PETER

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: BELMARES, MICHAEL P.

APPLICANT: BELMARES, MICHAEL P.

APPLICANT: BIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: SCHWEIZER, JOHANNES

FILE OF INVENTION: AND METHODS OF THEIR USE

FILE REFERENCE: VITA-012

CURRENT APPLICATION NUMBER: US/11/021,949

CURRENT APPLICATION NUMBER: 60/532,373

PRIOR APPLICATION NUMBER: 60/532,373

PRIOR APPLICATION NUMBER: 60/532,373

PRIOR APPLICATION NUMBER: 60/532,373

PRIOR FILING DATE: 2003-12-23

1 NUMBER OF SEQ ID NOS: 361

SOPTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 23
LENGTH: 155
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.7%; Score 379; DB 6; Length 154; Best Local Similarity 51.1%; Pred. No. 1.2e-32; Matches 72; Conservative 20; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 21
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                             ORGANISM: human papilloma virus (HPV)-11-021-949-23
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 154
TYPE: PRT
                                                                                                                                                                                                                         Local
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                                                                                                                                            1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                             h 44.9%; Score 372.5; DB 6; Length 155; Similarity 50.7%; Pred. No. 6e-32; 76; Conservative 20; Mismatches 53; Indels 1
AVCRVCLLFYSKVRKYRYYKYSVYGATLESITKKOLSDLSIRCYRCQCPLTPEEKQLHCE
                               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                               IFSNTQERPRSLHHLSEVLQIPLLDLRLSCVYCKKELTSLELYRFACIELKLVYRNNWPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVCKFCLLFYSKVRKLRYYNCSVYGASLEALTKKKLSDLSIRCYRCQHPLTPEEKQLHCD
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                                                                                                                                                                                               Gaps
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123
                                                                                                                                                 60
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RESULT 69
US-10-751-845-157
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US-10-751-845-126
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US-10-751-845-126
                                                                                                                PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 157, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 126, Application US/10751845 Publication No. US20050100928A1
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APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
FILE REFERENCE: 08191-013001
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/154,665 PRIOR FILING DATE: 1999-09-16
FEATURE: OTHER INFORMATION: Artificial fusion sequence
                                                  ORGANISM: Artificial Sequence
                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 40.1%;
Local Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 HKRRFHYIAYAWTGSCLQCWRHT-SRQATE 152
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o. US20050100928A1
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Pred. No. 8e-28;
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APPLICANT: Chicz, Roman M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPTIDES
FILE REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 163
SOFTWARE: FRST SEQ for Windows Version 4.0
SEQ ID NO 158
LENGTH: 237
TYPE: PRT
COEMING ALLIFICATE SECURCE
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hedley, M
APPLICANT: Urban, R
APPLICANT: Chicz, R
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Best Local Similarity
Matches 66; Conserv
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              TITLE OF INVENTION: NUCLEIC ACIDS ENCODING FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR PILING DATE: 2000-00-18
PRIOR PILING DATE: 1099-12-09
PRIOR FILING DATE: 1999-12-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Artificial fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
APPLICATION NUMBER: US 60/154,665
                                                                                                                                                                                                                                                                                                                                                                             46
                                                                                                                                                                                                                                                                                                                                                                                                        61 AVXDXCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLI 101
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|-----KISEYRHYCYSLYGTTLEQQYNKTLHEYML 74
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                                                                                                                                                                     Urban, Robert G.
Chicz, Roman M.
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5. US20050100928A1
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                                                                                                                                                                                                Mary Lynne
Robert G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 333; DB 5;
Pred. No. 1.8e-27;
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Pred. No. 1.8e-27;
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                                                                                                                                                          POLYEPITOPE POLYPEPTIDES
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; FEATURE: ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-160
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US-10-367-095-10
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                                                                                                                                                                  OTHER INFORMATION: HPV-16 L2/E6 fusion protein US-10-367-095-10
                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10367095 Publication No. US20030228696A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 160
LENGTH: 261
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Best Local :
                                                                                  Matches
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                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 44149-1US1
CURRENT APPLICATION NUMBER: US/10/367,095
CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/356,154
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Robin A. Robinson TITLE OF INVENTION: No. US20030228696Alel Insect Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/356,113
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                      MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 59
MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP
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                                                                             38.9%; Score 323; DB 4;
100.0%; Pred. No. 5.5e-26;
tive 0; Mismatches 0;

    Mismatches

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Pred. No. 2e-27;
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US-10-368-046-10
FILE REFERENCE: 44149-2US1
CURRENT APPLICATION NUMBER: US/10/367,367
CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,113
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR APPLICATION NUMBER: US 60/356,157
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CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
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Best Local (
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SEQ ID NO 10
LENGTH: 536
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Robin A. Robinson
TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Virus-Like Particles for Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/356,135 PRIOR FILING DATE: 2002-02-14
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PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robin A. Robinson APPLICANT: Vittoria Cioce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/356,123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/356,154 FILING DATE: 2002-02-14
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FILING DATE: 2002-02-14
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FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
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No. US20040063188A1
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Pred. No. 5.5e-26;
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US-10-918-337-10
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                                                                                                                                                            ; OTHER INFORMATION: HPV-16 L2/E6 fusion protein US-10-918-337-10
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
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PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
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                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: PCT/US03/04473
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 60/356,119
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PRIOR APPLICATION NUMBER: US 60/356,161
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TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Chimeric Virus-Like Particles for
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/356,154 PRIOR FILING DATE: 2002-02-14
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PRIOR APPLICATION NUMBER: US 60/356,133
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                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                         1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 59
                                                                               Conservative
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Pred. No. 5.
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                                                                                                                                   ) OTHER INFORMATION: Artificial fusion sequence US-10-751-845-159
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SEQ ID NO 11
LENGTH: 150
                                                               Query Match
Best Local Similarity
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                                               Matches
                                                                                                                                                                                                                                                                       SEQ ID NO 159
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ORGANISM: Homo sapiens
-10-367-057-11
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITORE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Urban, Robert G
APPLICANT: Chicz, Roman M
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APPLICANT: Ooi, Chean Eng
TITLE OP INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
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APPLICANT: Jackson, Amand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ublication No.
                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKK 122
8 RPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCL 67
                                            48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackson, Amanda;
Lewin, David A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10751845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mary Lynne
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                                                                 22.8%;
                                        ; Score 189; DB 5; I
; Pred. No. 2.9e-12;
14; Mismatches 32;
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                                                                                    Length 119;
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                                          Indels 42;
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                                          Gaps
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICI
APPLICANT: MAILLERE, Bernard
APPLICANT: MOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
ITILE OF INVENTION: Mixcure of peptides derived from E6 and/or E7
ITILE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR RILING DATE: 2002-05-03
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-04
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAUTT-VILLADA, Isabelle
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SEQ ID NO 19
LENGTH: 33
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CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILLING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                        APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 63
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Pred. No. 1.3e-11;
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US-10-476-570-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Mixture of peptides derived from E6 and/or TITLE OF INVENTION: papillomavirus proteins and uses thereof FILE REFERENCE: 45636-5071-US CURRENT APPLICATION NUMBER: US/10/476,570 CURRENT FILING DATE: 2003-11-04 PRIOR APPLICATION NUMBER: PCT/FR02/01533 PRIOR FILING DATE: 2002-05-03 PRIOR PILING DATE: 2002-05-03 PRIOR APPLICATION NUMBER: FR 01 05980 PRIOR FILING DATE: 2001-05-04 NUMBER OF SEQ ID NOS: 63 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 53
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LENGTH: 32
TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10858384
Publication No. US20050033025A1
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Best Local Similarity
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Best Local Similarity
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
ITILE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF PPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
THE REFERENCE: 0508-1037-1
CURRENT PILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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100.0%; F1
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100.0%; Pred. No. 3.9e-10;
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; Pred. No. 4.5e-11
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; DUBLICANT CHOPPIN, JEANNINE
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 F
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: POUVELLE-MORNTILLE, SANGEAR

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: papillomavirus proteins and uses thereof

FILE REFERENCE: 45636-5071-US

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT FILING DATE: 2003-11-04

PRIOR APPLICATION NUMBER: PCT/FR02/01533

PRIOR APPLICATION NUMBER: FR 01 05980

PRIOR APPLICATION NUMBER: FR 01 05980

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 55
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                                                                                                                                                                                                                                                                                                             RESULT 83
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Best Local Similarity
Matches 30; Conserv
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 4
                                                                                                                                                                                                                                                Sequence 8, Application US/10858384 Publication No. US20050033025A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment OTHER INFORMATION: for E6 of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION: Description of the artificial sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                       ISEYRHYCYSLYGTTLEQQYNKPLCDLLI 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 159; DB 4
Pred. No. 1e-09;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 8
LENGTH: 29
LENGTH: 29
LENGTH: 29
TYPE: PRT
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                                                                                                         Sequence 5, Application US/11021949
Publication No. US20050142541A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13
LENGTH: 29
TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                         GENERAL INFORMATION
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Best Local Similarity
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUVELLE-MORATILLE, Sandra
APPLICANT: BOUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment OTHER INFORMATION: for E6 of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                        84 YGTTLEQQYNKPLCDLLIRCINXQKPLCP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ISEYRHYCYSVYGTTLEQQYNKPLCDLLI 101
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                                                                                                                                                                                                                                              1 YGTTLEQQYNKPLCDLLIRCINCQKPLCP 29
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                                                                                                                                                                                                                                                                                                                                                        Score 157; DB 4; Length 29; Pred. No. 1.7e-09;
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FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 24
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-23
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                                                                   US-11-021-949-1
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                                                                                     RESULT 87
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Publication No. US20050100554A1
GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
Sequence 1, Application US/11021949 Publication No. US20050142541A1 GENERAL INFORMATION:
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.4%; Score 136.5; DB 5; Best Local Similarity 28.0%; Pred. No. 1.7e-06; Matches 37; Conservative 21; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 198
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                               130 GRWTGRCMSCCR 141
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                                                                                                                                                                                                                                                                                   70 YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
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24; Conserv
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Pred. No. 2.1e-08;
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APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAV
APPLICANT: BELMARES, MICHAEL P.

JONATHAN DAVID

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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
ITILE OF INVENTION: Maxture of peptides derived from E6 and/or E7
ITITLE OF INVENTION: Maxture of peptides and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 40
LENGTH: 23
TWARE: Patentin Ver: 2.1
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US-10-476-570-40
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                                                                                                                      US-10-476-570-44
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                                                     Sequence 44, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
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LENGTH: 25
TYPE: PRT
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Best Local Similarity
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
APPLICANT: MAILLERE, Bernard
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PASTSEQ for Windows Version 4.0
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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23; Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                           3e-07;
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                   LA RECHERCHE MEDICALE
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; Sequence 56, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE
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                                                                                                               US-10-476-570-56
                                                                                                                                      RESULT 91
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                                                                                                                                                                                                                                                                                            Query Match 15.9%; Score 132; DB 5; Best Local Similarity 100.0%; Pred. No. 6.7e-07; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLERIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerack
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/154,665 PRIOR FILING DATE: 1999-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: FR 01 05980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 IRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                     37 LLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                           1 LLRREVYDFAFRDLCIVYRDGNPY 24
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100.0%; Pred. No. 3.
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3.2e-07
    5
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APPLICANT: COOPEN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: TO SECONDATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIAN OF SECONDATE: 1999-06-03
LENGTH: 22
TYPE: PRT
DROANISM: Artificial Sequence
FEATURE:
CTUER IN PROCENTION DESCRIPTION OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTIFICIAL OF THE ARTI
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APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: papillomavirus proteins and uses thereof

FILE REFERENCE: 45636-5071-US

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT FILING DATE: 2003-11-04

PRIOR APPLICATION NUMBER: PCT/FR02/01533

PRIOR FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 56

LENGTH: 22

TYPE: PRT

ORGANISM: artificial sequence

FEATURE:
RESULT 93
US-10-751-845-152
; Sequence 152, Application US/10751845
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; OTHER INFORMATION: for E6 of HPV
US-10-858-384-10
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Best Local &
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Best Local Similarity
Matches 22; Conserv
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22; Conserv
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BOURGAULT-VILLADA, Isabelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
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APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/9/664,225
PRIOR FILING DATE: 1090-08-18
PRIOR PILING DATE: 1909-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-19-16
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US-10-751-845-66
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CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 23
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 42
                                                                                                 Query Match
Best Local Similarity
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Publication No. US20050100928A1
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Best Local Similarity
                                                                                    Matches
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APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLERIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
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                    72 KISEYRHYCYSVYGTTLEQQYNK 94
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KISEYRHYCYSLYGTTLEQQYNK 23
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                                                                                                      15.2%; Score 126; DB 5; 95.7%; Pred. No. 2.9e-06;
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Pred. No. 2.1e-06;
6; Mismatches 11
                                                                                      Mismatches
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RESULT 95
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

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; NUMBER OF SEQ ID NOS: 361
; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-3
                                                                               RESULT 97
US-10-476-570-27
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Best Local S
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CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Patentin Ver. 3.2
SEQ ID NO 6
LENGTH: 22
TYPE: TATE
                                 GENERAL INFORMATION:
                                               Sequence 27, Application US/10476570 Publication No. US20040170644A1
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Best Local Similarity
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
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TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE TITLE OF INVENTION: PARTICULARLY IN VACCINATION FILE REFERENCE: 0508-1037-1
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 RREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                          99 LLIRCINXQKPLCPEEKQRHLDK 121
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                                                                                                                                                      1 LLIRCINCOKPLCPEEKORHLDK 23
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CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOURGAULT VILLADA,
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; Pred. No.
                                                                                                                                                                                                                                      Score 119; DB 6;
Pred. No. 1.6e-05;
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                                                                                                                                                                                                                                                    DB 6; Length 23;
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APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 23
TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-938-249-513
                                                             Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 543
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 513, A Publication No.
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/938,249
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US/09/724,553
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/134,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/196,267 PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                  PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/176,195
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/170,453
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/134,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 020054-001130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schweizer, Johannes
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ORGANISM: Artificial Sequence
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3, Sandra
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Pred. No. 3.9e-05;
0; Mismatches (
                                                                                                                                   See File Wrapper or PALM
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Sequence 4, Application US/10612818

Publication No. US20040110925A1

GENERAL INFORMATION:

APPLICANT: Impact Diagnostics

APPLICANT: Impact Diagnostics

TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse

TITLE OF INVENTION: Associated Cancers

FILE REFERENCE: 3352-2-2

CURRENT APPLICATION NUMBER: US/10/612,818

CURRENT APPLICATION NUMBER: US 60/394,172

PRIOR APPLICATION NUMBER: US 60/394,172

PRIOR APPLICATION NUMBER: US 09/828,645

PRIOR FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MAILLERE, Bernard

APPLICANT: MAILLERE, Bernard

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: papillomavirus proteins and uses thereof

FILE REFERENCE: 45636-5071-US

CURRENT APPLICATION NUMBER: BCT/FR02/01533

PRIOR APPLICATION NUMBER: BCT/FR02/01533

PRIOR APPLICATION NUMBER: BCT/FR02/01533

PRIOR APPLICATION NUMBER: BCT/FR02/01533

PRIOR APPLICATION NUMBER: BCT/FR02/01533

PRIOR FILING DATE: 2001-05-03

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 41

LENGTH: 20

TYPE: PRT

ORGANISM: artificial sequence

PEATURE:

COURSE TROOD AND TO SECULOTION OF THE ARTIFICIAL SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF THE SECULOR OF T
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US-10-476-570-41
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 13.9%; Score 115; DB 5; ]
Local Similarity 100.0%; Pred. No. 3.7e-05;
hes 20; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.8e-05;
tive 0; Mismatches 0;
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Perfect score:
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Gapop 10.0
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Match
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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163.129 Million cell updates/sec
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GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of
TITLE OF INVENTION: Milk
FILLE FEBERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
CURRENT APPLICATION NUMBER: 2004-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of Fus
TITLE OF INVENTION: Milk
FILE REFERENCE: GTC-220 PCT
CULLENT APPLICATION NUMBER: US/10/933,854
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-10-933-854-6
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LENGTH: 591
TYPE: PRT
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                      SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10933854 Publication No. US20060105347A1
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NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Accession No.
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
                                     PRIOR APPLICATION NUMBER: 60/500,910 PRIOR FILING DATE: 2003-09-05 NUMBER OF SEQ ID NOS: 35 SOFTWARE: Patentin version 3.2
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Similarity 23.4%; Pred. No. 1.6;
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NAME/KEY: misc feature

OTHER INFORMATION: Human Alpha Fetoprotein

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Genbank/Accession

DATABASE ENTRY DATE: 1995-03-30

RELEVANT RESIDUES: (1)..(609)

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Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Blotherapeutics, Inc.
APPLICANT: CCx, Geoffrey F.
APPLICANT: Ccx, Geoffrey F.
APPLICANT: Meade, Harry
APPLICANT: Meade, Harry
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APPLICANT: Meade, Harry
APPLICANTON MILK
TITLE OF INVENTION: Milk
FILE REFERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
CURRENT APPLICATION NUMBER: 60/500,910
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR FILING DATE: 2003-9-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 260
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Best Local Similarity
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DATABASE ACCESSION NUMBER: Genbank/Accession
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
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FEATURE:
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OTHER INFORMATION: Human Alpha Fetoprotein
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Local Similarity 23.4%;
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                                        INXQKPL-C---PEEKQRHLDKKQ 123
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ilarity 23.4%;
Conservative 2
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                                                                                                                                                                                                                                                                             Score 74.5;
Pred. No. 1.
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Pred. No. 1.6;
                                                                                                                                                                                                                                                           Mismatches
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RESULT 5
US-10-953-349-33870
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US-10-953-349-33870
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SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 33870
LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33870, Application US/10953349
Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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LENGTH: 800
TYPE: PRT
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Best Local 9
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Best Local Similarity 23.3%; Pred. No. 3.
Matches 34; Conservative 22; Mismatche
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FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 ---NPVGGNEKCADVTIHIFFSKILKLAAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 573
                                                                                                                                                                           469 DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574 TLFFNRHIDQLILCCLYGVAKVCQLE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                   55 RDGNPYAVXDKCLK----FYSKISE----YRHYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY 54
                                                                                                                                                                                                                     4 DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY 54
TLFFNRHIDQLILCCLYGVAKVCQLE 608
                                          ---YNKPLCDLLIRCINXQKPLCPEE 114
                                                                                      ---NPVGGNEKCADVTIHIFFSKILKLAAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YNKPLCDLLIRCINXQKPLCPEE 114
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23.3%; Pred. No. 3.6;
vative 22; Mismatches
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                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                    49; Indels
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                                                                                                                                                                                                                                                                                                              Length 809;
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                                                                                                                              ----YSVYGTTLEQQ-
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2762
LENGTH: 531
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; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33869
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US-10-953-349-33869
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PATENTIN VERSION 3.3
SEQ ID NO 33869
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2762, Application US/11293697 Publication No. US20060105376A1
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Best Local Similarity
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
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271 DRNKETR 277
                                     144 RTRRETQ 150
                                                                                                                                                      175 LGCFKCKSCGKLLNAE-----YISKDGLPYCEADYHAKFGIRCDSCEKY---ITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 TLFFNRHIDQLILCCLYGVAKVCQLE 666
                                                                                                               86 TTLE--QQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 ---YNKPLCDLLIRCINXQKPLCPEE 114
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                                                                            RVLEAGEKHYHPSCALCVGC---
                                                                                                                                                                                                                                  8.6%; Score 71; DB ilarity 22.0%; Pred. No. 3.3; Conservative 16; Mismatches
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23.3%; Pred. No. 3.9;
ative 22; Mismatches
                                                                          -GOMFAEGEEMYLOGSSIWHPACROAARTE
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US-10-953-349-6306
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 17182
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6306
LENGTH: 419
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
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CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
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301
                                                                                                                                                             194
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                                                                             254 VCI----GNPGSLTDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPLTDYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 WFKEVEKIIQPLFKEIKDSQGRTPQMLFTEEHKELAKEGE----
                                                                                                                   50 LCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
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                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLL-------RRE--
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Similarity 22.2%;
39; Conservative 2
LVPYTRQNLTWTQHAFNESIGEIQGIATAAFERLKGRW-----ACLQKRTEVKLQ
                                     LCPEEKQ----RHLDKKQ-----
                                                                                                                                                             ESVHKIPNVVGSIYTTHIPIIAPKVHVAAYFNKRHTERNQKTSYSITVQGVVNADGIFTD
                                                                                                                                                                                                ERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KPLCDLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRCMSCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNLIYDIGAHKDLITSYRDNNNHNI----LHLAGKLAPSEQLHV---VSGAALQMQRELL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VYDF-AFRDLCIVYRDGNPYAVXDKCLKFYSKI--SEYRHYCYSVYGTTLEQQYN--
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                           7.7%; Score 63.5;
21.0%; Pred. No. 16;
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                                     ---RFHNIRGRWTGRCMSCCRSSRTRRETQ
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Sequence 6305, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579 PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 6304
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Best Local Similarity
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Publication No. US20060107345A1
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Best Local
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                                110 LCPEEKQ-----RHLDKKQ------RFHNIRGRWTGRCMSCCRSSRTRRETQ 150
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LVPYTRONLTWTQHAFNESIGEIQGIATAAFERLKGRW----
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21.0%;
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                                                                                                                                                                                                                                 19; Mismatches
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Pred. No. 20;
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CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 32520
LENGTH: 276
TYPE: PRT
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US-10-953-349-32519
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US-10-953-349-32520
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
Sequence 32519, Application US/10953349
publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 32521
LENGTH: 247
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19; Conserv
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Similarity 25.7%;
19; Conservative 1
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Pred. No. 11;
11; Mismatches
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US-11-293-697-4876
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn vers
SEQ ID NO 32519
LENGTH: 307
TYPE: PRT
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US-11-293-697-4876
                                                                                                                                                                         Sequence 8, Application US/11106014 Publication No. US20060088846A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4876
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APPLICANT: HELIX RESEARCH INSTITUTE
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            APPLICANT: Srivastava, Promod
APPLICANT: Chandawarker, Rajiv
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-106-999
                                                                         APPLICANT: Pagano, Michele
APPLICANT: Chiaur, Dah Sharim
APPLICANT: Latres, Esther
APPLICANT: Srivastava, Promod
APPLICANT: Chandawarker, Rajiv
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CURRENT APPLICATION NUMBER: US/11/106,014
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Local Similarity 22.3%;
nes 33; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ---YSVYGTTLEQQYNKPLCDLLI------RCINXQKPLCPE-----EKQRHLDKKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 CVYCKQQLLRREVYDFAF-----RDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYC---
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25.7%;
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Pred. No. 13;
18; Mismatches
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Pred. No.
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RESULT 17
US-10-196-749-474
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PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/196,749

CURRENT FILING DATE: 2002-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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PRIOR FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR FILING DATE: 1997-03-15
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PRIOR APPLICATION NUMBER: 10/042,417
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 09/385,219
PRIOR FILING DATE: 1999-08-27
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PRIOR APPLICATION NUMBER: 10/632,150
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                  APPLICATION NUMBER: 60/063486 FILING DATE: 1997-10-21
                                                                                                            FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063121
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063540 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063541
                                                                                                                                                                              FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/063120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 FGPRLEQ----LNTSLVLSLLSSEELCPTAGLPQRQID 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 YGTTLEQQYNKPLCDLLIRCINXQKPLCPEE--KQRHLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J. Gurney, Austin L.
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Goddard, Audrey
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; Pred. No. 22;
14; Mismatches
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-225
                                                         ; LENGTH: 176
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18091
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Best Local Similarity
Matches 17; Conserv
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PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 474
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SEQ ID NO 225
LENGTH: 1056
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  Best Local Similarity
                      Query Match
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
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TYPE: PRT
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7.4%;
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Pred. No.
  Score 61.5; D
Pred. No. 9.9;
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US-10-953-349-18090
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US-10-953-349-18090
                                                                     ; ORGANISM: Glycine max US-10-953-349-18089
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                                                                                                                   Sequence 18089, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXAUROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 18089

LENGTH: 220
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LENGTH: 208
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Query Match 7.4%;
Best Local Similarity 21.6%;
Matches 27; Conservative 1
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 WTGRC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 YGTTLEQQY--NKPLCDLLIRCINXQKPLCPEEKQRHLDKKQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 VRTVLHQLYEMNPPKYTWFYNFVASNKPADGKRFIRSLGKEQQELAERVMVTRLH-LYGK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 YGTTLEQQY--NKPLCDLLIRCINXQKPLCPEEKQRHLDKKQ------RFHNIRGR 131
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21.6%; Pred. No. 12;
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Score 61.5; D
Pred. No. 13;
11; Mismatches
                                DB 6;
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   44;
                                  Length 220;
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   Indels
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Sequence 19918, Application US/10953349
Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 19918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4346
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US-11-293-697-4346
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US-10-953-349-19918
                                                                                                                                                                               ; ORGANISM: Glycine max 
US-10-953-349-19918
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4346
LENGTH: 705
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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                                                                                                                                   Query Match
                                                                                                                                                                                                                        LENGTH: 25
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 XQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 DLLIHKSIHTGEQPYKC-DECEKVFSRKSSLETH---KIGHTGEKPYKCKVCDKAFAC-- 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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                                              18
                                                                                       l Similarity
29; Conserv
                                                                                                                                                                                                                                               259
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Similarity 24.7%; Pred. No. 44;
24; Conservative 13; Mismatches
DILSTLADVALEREDFETSLSDYQKALTILEQLVEPDDRNIADLNFR-ICL-----
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                                           ELQTTIHDIILE----
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                                                                                         Conservative
                                                                                       7.3%; Score 61; DB 20.9%; Pred. No. 17; tive 23; Mismatches
                                           --CVYCKQQLLR---REVYDFAFRDLCIVYRDGNPYA
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                                                                                                                                   Length 259;
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; Sequence 28497, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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US-10-953-349-19917
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                                                                                                                                                               APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 28497
LENGTH: 267
TYPE: PAT
ORGANISM: Triticum aestivum
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 19917
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TYPE: PRT
                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 SESNNSILDKOSEIETLKG 239
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   40
                                    11 KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAF------RDLCIVYRDG 57
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   KFPSLPPVFQQTPNAV-----EELKLAREIYEQAVILSVKMEDQDAFERDFCQL----
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                                                                             Conservative
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                                                                                          7.3%;
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                                                                         Score 60.5; D
Pred. No. 20;
20; Mismatches
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                                                                                                           Length 267;
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FILE REFERENCE: H1-A0106

CURRENT FAPPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3919

LENGTH: 706

TYPE: PRT
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; SEQ ID NO 365
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-365
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US-11-293-697-3919
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                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-293-697-3919
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Publication No. US20060094649A1

GENERAL INFORMATION:

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7

TITLE OF INVENTION: Peptides and Compositions

FILE REFERENCE: 2060.015PC06

CURRENT APPLICATION NUMBER: US/10/538,066

CURRENT FILING DATE: 2005-06-09

CURRENT FILING DATE: 2005-06-09
                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/432,017 PRIOR FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 LESVLRNCQDFFPVIFSKASEYLQLVFGIEVVEVVPISHLYILVTCLGLSYDGLLGDNQV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 NPYAVXDKC-----HYCYSVYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
l Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPKTGLLIIVLAIIAIEGDCAPEEK 220
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                                                           Conservative
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                                              7.3%; but
20.7%; Pred
tive 22;
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                                                         Score 60.5; DE Pred. No. 56; 22; Mismatches
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Pred. No. 23;
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                                                                                             DB 7;
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                                                                                               Length 706;
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                                                         Indels
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                      42
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US-10-505-928-397
                                                                                                                                                                                                                                                                  Sequence 175, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
                                                                                                                     SEQ ID NO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 866
SOPTWARE: PatentIn 3.2
SEQ ID NO 397
LENGTH: 971
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  Query Match
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                                                                                                                                PKIUK FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
                                                                                                                                                                          CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/505,928
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CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                       FILE REFERENCE: 28967/39178
                                                        TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                               LENGTH: 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 DSLYCCDRAEDH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 THGSGGRFKCQV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 CCELA----IALECRQACKQASSKNDISKVCRKEYENALFS--CISRNE-----MGSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LKFYSKISEYRHYCYSVYGTTLE-----QQYNKPLCDLLIRCIN-----X
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5. US20060088532A1
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Pred. No. 79;
22; Mismatches
  Score 60.5;
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Length 1085;
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RESULT 31
US-10-953-349-13389
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                             Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13389
LENGTH: 233
                                                                                                                                                                                                                                                                                                                      Sequence 13389, Application US/10953349
Publication No. US/20060107345A1
GENERAL INFORMATION:
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SEQ ID NO 3034
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                 APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                  TYPE: PRT
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KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA----FRDL-----CIVY 54
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                                   21; Mismatches
                                                   Score 59; DB Pred. No. 24;
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                                                                 Length 233;
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                                 Gaps
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1032
LENGTH: 258
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-1032
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                                                                                                                                                                               ; LENGTH: 369
; TYPE: PRT
; ORGANIZSM: Arabidopsis thaliana
US-10-953-349-1031
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US-10-953-349-1032
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1031
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Best Local
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Best Local
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TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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                                                  163 MAPDPPE-PQDLPEIC-----RDVMME--YSKQVMILGE---FLF-ELLSEALGLNPN
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               61 AVXD-KCLKFYSKISEYRHYCYS---VYGTT 87
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<u>:</u>
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                                                                                                                ; Score 59; DB; Pred. No. 40; 14; Mismatches
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   RESULT 36
US-10-953-349-13387
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; ORGANISM: Arabidopsis thaliana US-10-953-349-1030
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 13388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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SEQ ID NO 1030
LENGTH: 376
TYPE: PRT
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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nes 27; Conservative
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  291
                                                                                           236 AGRLESSPYSELLSPIHWEMTTEELARQFC----TLLGQSYENPLSVAVAAGVEGLPIL
                                                                                                                                                                                    178 KLVQIGSNLELKÍH--TLQFVEVLQNGTRADALKYARTYLAPFASLNKGEFPKLMGCLLÝ 235
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                                                                                                                                    55 R----DGNPYAVXDKCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPL------CDLL 100
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                                             IRCIN---XQKPLCPEEKQR----HLDKKQRFHNI 128
LKLANVMAAKKOEWOEMKOLPVPVELGKEFOFHSI 325
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Pred. No.
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 13387
LENGTH: 400
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                               Sequence 25007, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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SEQ ID NO 25008
LENGTH: 428
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-10-953-349-25008
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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CURRENT FILING DATE: 2004-09-30
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llarity 28.9%;
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; TYPE: PRT; ORGANISM: Glycine max US-10-953-349-25006
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                                                                                                                                                                                                                                                             ; ORGANISM: Zea mays subsp. mays
US-10-953-349-37463
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNDBER: US/10/953,349
CURRENT APPLICATION UNDBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATEING SOFTMARE: PATE
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 25006
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Best Local Similarity
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SOFTWARE: PatentIn version:
SEQ ID NO 25007
LENGTH: 433
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Publication No. US20060107345A1
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Best Local Similarity
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les 13; Conserv
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                                                          121 KKORFHNIRGRWTGR--
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94 QRORGHH-RARGISRRGWRRCSFASPRCSCSCLSCCRRCRRRR 135
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; Pred. No. 24;
4; Mismatches
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Pred. No. 48;
9; Mismatches
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Pred. No. 47;
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                                                              CMSCCRSSRTRR 147
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Sequence 38140, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40522
SOFTWARB: PATENTIN VERSION 3.3
SEQ ID NO 38140
LENGTH: 251
TYPE: PRT
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US-10-953-349-38140
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FULE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 38139
                                                    APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22153
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Best Local Similarity
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ORGANISM: Glycine max
                                       ENGTH: 421
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Pred. No. 33;
4; Mismatches
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Pred. No. 30;
4; Mismatches
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOSTWARE: Patentin version 3.3
SEQ ID NO 22151
LENGTH: 492
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DN
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22152
LENGTH: 471
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22152
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US-10-953-349-22151
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                                                                       Query Match
Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
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                                    45 FAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYC-YSVYGTTLEQQYNKPLCDLLIRC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSCENIC----GNPVPCGN-------HYCTKTCHALENQLQGSQPCEDCYLSC
 FSCENLC--
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                                                                                        7.0%;
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22.9%; Pred. No. 59;
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                                                                       Score 58.5; Di
Pred. No. 61;
11; Mismatches
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Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HYCTKTCHALENQLQGSQPCEDCYLSC 228
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                                                                                                            DB 6;
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HYCTKTCHALENQLÓGSQPCEDCYLSC 249
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                                                                         32;
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                                                                                                            Length 492;
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                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                         AND CORRESPONDING POLYPEPTIDES
                                                                         31;
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US-11-170-482-16
; Sequence 16, Application US/11170482
; Publication No. US20060094037A1
; GENERAL INFORMATION:
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US-10-953-349-24130
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                                                                                                                                                                                                                                            Sequence 24130, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCOUNCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCOUNDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 24130
LENGTH: 152
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                                                                                                                                     Query Match
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APPLICANT: Fraser, Paul E.
APPLICANT: University of Toronto
TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
FILE REPERENCE: 1034/1H570
CURRENT APPLICATION NUMBER: US/11/170,482
CURRENT FILING DATE: 2005-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/229,889
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US/09/945,258
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                                                                              TYPE: PRT
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                                                                          7.0%; Score 58; DB
Local Similarity 26.8%; Pred. No. 20;
hes 19; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 NXOKPLCPEEKORHLDKKORFHN--IRGRW----TGRCMSCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 NNSWFQSILKHDLRSY-LDDRPLQHYIAVS-----SPTNTTYVVQY--ALANLTGKAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 WQSPEEDLNFVTDTAKALANVATVLARALYELAGGTNFSSSIQADPQTVTRLLYGFLVRA
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  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                        88 LEQQYNKPLCDLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC----MSCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FQDPQE-----RPRKLPQLCTELQTTIHDI----ILECVYCKQQLLRREVYDFAFRD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708
LNEEMNKGLLTMLSEELNLQKIVANETMEHTKQLIMDARKTFSHYQ-KEAEKCNIGVETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTREQCQDPSKVPNESKDLYEYSWVQGPWNSNRTERLPQCVRST 623
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21.2%; Pred. No. 9:
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                                                                                                                                   DB 6; Length 152
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RESULT 50
US-10-953-349-22948
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Publication No. US20060107345A1

GENERAL INFORMATION: US20060107345A1

APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY

FILE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 24129

LENCYPUS 177
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22949
LENGTH: 264
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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Best Local (
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ORGANISM: Glycine max
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                                                                                                                                                                   39 QYKNTTĹPQ--TTĹKŤSVKELDĹÉAALAEREĹHVKĹŔKÉAAĎ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LEQQYNKPLCDLLIRCINXQKPLCPE----EKQRHLDXKQRFHNIRGRWTGRC---MSCC 140
                                                                                                                        63 XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPL-CP-EEKQRHLD 120
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                                                                                 --KITKLRRNV-EMDEYDYMHWRRSFEER-----EALTRDISCRKALGLPLEEPGRYMD
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26.8%; Pred. No.
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                                                                                                                                                                                                                                                                                         6; Length 264;
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22948, Application US/10953349

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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENCIN VERSION 3.3
SEQ ID NO 22312
LENGTH: 390
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22312
                                                                                                                                            RESULT 52
US-10-953-349-22947
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US-10-953-349-22312
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Sequence 22947, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PELLORICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22948
LENGTH: 359
TYPE: PRT
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXAMDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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GENERAL INFORMATION:
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-10-953-349-22948
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les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 QYKNTTLPQ--TTLKTSVKELDLEAALAERELHVKLRKEAAD------RGEKY-- 178
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                                                                                                                                                                                                                                                                                      --FHNIRGRW 132
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                                                                                                                                                                                                                                                                                                                                                                                    EYRHYCYSVYGTTLEQ-----QYNKPLCDLLIRCINXQKPLC-PEEKQRHLDKKQR- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                   TKMQAEIQKIDDE----VNEMKLKNEEEKLAIQDLEMALIKRRK----AEKCRRLAEAQS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELOTTIHDIILECVYCKQQLLRREVYDFAFRDL--CIVYRDGNPYAVXDKCLKFYSKIS 74
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22947
LENGTH: 393
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22311
LENGTH: 423
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                                                                                                                                                                    Sequence 21322, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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Best Local S
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               APPLICANT: ALEXANDROV, Nickclai et al.
TITLE OF INVENTION: SEQUENCE-BERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FAPILCATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                              159 DIEKQIRPEW 168
                                                                                                                                                                                                                                                                                                                                                                         125 -- FHNIRGRW 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYRHYCYSVYGTTLEQ------QYNKPLCDLLIRCINXQKPLC-PEEKQRHLDKKQR- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKMQAEIQKIDDE----VNEMKLKNEEEKLAIQDLEMALIKRRK----AEKCRRLAEAQS
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23.1%; Pred. No. 66;
ative 19; Mismatches
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; Sequence 22310, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRJ
; TITLE OF INVENTION: ENCONDED THERBY
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579BUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
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US-10-953-349-22310
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US-10-953-349-21321
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 21321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21321, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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  SEQ ID
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22310
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TYPE: PRT
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Local Similarity 22.6%;
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                                                                                                                                                                                                                                                                                                              281 ALFAGOHTSSITSTWIG 297
                                                                                                                                                                                                                                                                                                                                                                                           226 ----RDQARKKLAEIFASIITSRKSASKSEEDMLQCFIDSKYKDGRSTTEAEVTGLLIA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 HLIILTASRC---LIGREVRDKLFDDVSALFHDLDNGMLPISVLFPYLPIPAHKR-----
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31; Conservative
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Pred. No. 67;
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                                                                                                                                    FRAGMENTS
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                                                                                                                                    AND CORRESPONDING POLYPEPTIDES
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Sequence 12540, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12540
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US-10-953-349-12540
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US-10-953-349-21320
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SOFTWARE: PatentIn version
SEQ ID NO 21320
LENGTH: 518
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Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
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Best Local Similarity
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TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 HDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 EYRHYCYSVYGTTLEQ------QYNKPLCDLLIRCINXQKPLC-PEEKQRHLDKKQR- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 TELQTTIHDIILECVYCKQQLLRREVYDFAFRDL--CIVYRDGNPYAVXDKCLKFYSKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
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                                                                                                                                                                                                                                                                                                                                                      ----QRFHNIRGRWTG 134
                                                                                                                                                                                                                                                                                                                                                                                         ----RDQARKKLAEIFASIITSRKSASKSEEDMLQCFIDSKYKDGRSTTEAEVTGLLIA 311
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Pred. No. 79;
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Pred. No. 82;
                                                                                                                                           DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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Sequence 3341 Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                      US-11-293-697-3341
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  Best Local Sin
Matches 29;
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Best Local Similarity 26.7%;
                                          Query Match
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APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/318,156
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2002-11-12
                                                                                                                                 LENGTH: 185
TYPE: PRT
                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 35.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 EEQYWDPLLGTCMSC----KTICNHQSQR----
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h 6.8%; Score 56.5; I Similarity 23.8%; Pred. No. 35; 29; Conservative 17; Mismatches
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Pred. No. 31;
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Pred. No. 55;
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                                          DB 7;
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                                          Length 185;
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Indels
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo &
US-11-318-156-2
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APPLICANT: Von Bolow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/11/318,156
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR PILING DATE: 1997-03-03
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                                                                                                                                               Sequence 3991, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOCTWARE: Patentin version 3.3

SEQ ID NO 3991

LENGTH: 516
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  Best Local Similarity Matches 19; Conserv
                                             Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                      LENGTH: 516
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
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16; Conserv
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  Conservative
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Score 56.5; DB 6;
Pred. No. le+02;
0; Mismatches 21;
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Pred. No. 57;
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                                             Length 516;
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  Gaps
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3990
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US-10-953-349-3990
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                                                                                                                                                       Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                   APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
RUMBER OF SEQ ID NOS: 40252
SOPTMARE: PRIENTING Version 3.3
SEQ ID NO 3989
LENGTH: 547
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3990, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCOUDED ETERBY
TITLE OF INVENTION: ENCOUDED THERBY
FILE REPERENCE: 2750-1579PUS2
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 SQSCVSSSR 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 SQSCVSSSR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 CMSCCRSSR 144
461 SQSCVSSSR 469
                                      136 CMSCCRSSR 144
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                                                                                                              78 HYCYSVYGTTLEQQ--YNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGR 135
                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 HYCYSVYGTTLEQQ--YNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGR 135
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                                                                           HYVYNNHGYSSEEETMYSAETAE----SRNYPTPP----RKSEFHHER---VGR
                                                                                                                                                         Conservative
                                                                                                                                                     6.8%; Score 56.5; DB 6; 27.5%; Pred. No. 1.1e+02; rative 10; Mismatches 21;
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                                                                                                                                                                                            Length 547;
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Sequence 3838, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3838
LENGTH: 968
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US-10-953-349-19251
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US-11-293-697-3121
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3121
LENGTH: 840
TYPE: PRT
                                                                                                                       Sequence 19251, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%; Score 56.5; DB 7; Best Local Similarity 21.7%; Pred. No. 2.1e+02; Matches 25; Conservative 17; Mismatches 42;
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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                                                                                                                                                                                                                                                                                                                                                                                               181 RKVROMFQEADTDENOGTLTFEEFCVFYKMMSLRRDLY-----LLLLSYSDKKDHLTVEE
                                                                                                                                                                                                                                                                                                 236 LAQFL-KVEQKMNNVTTDYCLDIIKKFEVSEENKVKNVLGIEGFTNFMRSPACDI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                               10 RKLPQLCTELQTTIHDIILE----CVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 YGTTLEQQYNKPLCDLLI------RCINXQKPLCPEEKQRHLDKKQRFHNI 128
                                                                                                                                                                                                                                                                                                                                               66 CLKFYSKISEYRH-----YCYSVYGTTLEQQYNK-------PLCDL
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14; Conserv
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26.4%; Pred. No. 1.8e+02;
ative 12; Mismatches 18
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US-11-259-950-95
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; ORGANISM: Glycine max
US-10-953-349-19251
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/536,281
PRIOR FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: US 10/465,789
PRIOR FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 60/252,233
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 11/033,489
PRIOR APPLICATION NUMBER: US 11/033,489
PRIOR FILING DATE: 2005-01-11
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19251
LENGTH: 233
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 95
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                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                           LENGTH: 279
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                   OTHER INFORMATION: Recombinant Tissue Factor with truncated .11-259-950-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/259,950
CURRENT FILING DATE: 2005-10-27
PRIOR APPLICATION NUMBER: US 60/622,737
PRIOR FILING DATE: 2004-10-27
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APPLICANT: Pureza, Vincent
APPLICANT: Sligar, Stephen G.
TITLE OF INVENTION: Tissue Factor Compositions
FILE REFERENCE: 46-04
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                                                                                                                                                                                     Match 6.7%;
Local Similarity 18.1%;
                                                                                 153
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                                   64 DKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQK 108
                                                                                                                     14 QLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLC---IVY-----RDGNPYAVX 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 KLPOLCTELQTTIHDIILECVYCKQQLLRREVYDFA-----FRDL------
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TNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMGQEK 249
                                                                                 QVGTKVNVTVED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGRLESSPYSELLSPIHWEMTTEELTRQFC----TLLGQSYENPLSVAVAAGVEGLPTL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLVQIGSNLELKIH--TLQFVEVLQNGTRADALKYARTYLAPFASLNKGEFPKLMGCLLY 83
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                                                                                                                                                                   Conservative
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                                                                               ---ERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAK 204
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                                                                                                                                                                 21; Mismatches
                                                                                                                                                                                     Score 56; DB Pred. No. 61;
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Sequence 19922, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19822
LENGTH. 2012
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCOMDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 19821
LENGTH: 303
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US-10-953-349-19821
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity
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les 28; Conserv
 116
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                                   147 RETQ 150
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                                                                         64
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                                                                                                                                                14 KHITEKDVYNLLSNEEHILGEESS-QSSNDK-----KINDLRERGYMKYGC---QHYRR
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                                                                                                                                                                                      35 QQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
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QEVQ 119
                                                                                                            ----PLCDLLIRCINXQKPLCPEEKQR--HLDKKQRFHNIRGRWTGRCMSCCRSSRTR 146
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                                                                         RCRIRAPCCDEIFDCRH---
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Conservative 23;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                         6.7%; Score 56; DB 22.6%; Pred. No. 66; ative 23; Mismatches
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                                                                         CHNEAKNNINIDQKHR-HDIPRHQVKQVI--CSLCETE
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RESULT

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US-10-953-349-6767
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-6767
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RESULT 73
US-10-953-349-19250
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 6767
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity 22.6%;
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
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                                                                                                                 90 Q 90
                                                                                                                                                                                         40 REVYDFAFRDLCIV-----YRDGNPYAVXDKCLKF--YSKISEYRHYCYSVYGTTLE 89
                                                                                                                                                                                                                                25 KRPKTLQQICRECFYEVFEEEIHQVIVQNRLFKSGERVAIGASGGKDSTVLAYVLSELNR
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                                                                                                                                                     RHNYGL---DLFLLSIDEGITGYRDDSLETVKRNEVQYGLPLKIVSYK--
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Pred. No. 79;
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US-10-953-349-19249
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US-10-953-349-19250
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 19250
LENGTH: 385
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 19249
LENGTH: 410
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
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                                          101 IRCIN---XOKPLCPEEKOR----HLDKKORFHNI 128
                                                                                    261
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                                                                                                                                                                 203 KLVOIGSNLELKIH--TLOFVEVLONGTRADALKYARTYLAPFASLNKGEFPKLMGCLLY 260
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37; Conserv
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37; Conserv
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                                                                                    AGRLESSPYSELLSPIHWEMTTEELTROFC----TLLGOSYENPLSVAVAAGVEGLPTL 315
                                                                                                                              R---DGNPYAVXDKCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPL---
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LKLANVMAAKKQEWQEMKQLPVPVELGKEFQFHSI
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RESULT 75 US-10-953-349-8916 ; Sequence 8916, Application US/10953349

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US-10-953-349-34190
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US-10-953-349-34190
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US-10-953-349-8916
Sequence 34189, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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LENGTH: 274
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SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                           258 QKTPVEQE 265
                                                                                                                                                                                                                                                                                                                                 36 QLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFY-----SKISEYRHYCYSV 83
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19.7%; Pred. No. 4:
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CURRENT APPLICATION NUMBER: US/10/5; CURRENT FILING DATE: 2004-09-30; NUMBER OF SEQ ID NOS: 40252; SOFTWARE: Patentin version 3.3; SEQ ID NO 34189; ENOTH: 278; TYPE: PRT ORGANISM: Zea mays subsp. mays US-10-953-349-34189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34188, Application US/10953349
Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DEFERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34188
LENGTH: 280
TYPE: PRT
                                                       APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DN
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 938
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US-10-953-349-938
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity 23.5%;
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Best Local
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LENGTH: 403
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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les 16; Conserv
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Conservative
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Pred. No. 69;
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Pred. No. 68;
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                                                                                                                                                                                          DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 937
LENGTH: 436
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-937
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                                                                     RESULT 82
US-10-953-349-936
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US-10-953-349-9969
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
               Sequence 936, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                      Matches
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LENGTH: 436
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CURRENT FILING DATE: 2004-09-30
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APPLICANT: ALEXANDROV, Nickolai et al
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                        Local Similarity
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Pred. No. 1.1e+02;
3; Mismatches 15
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Pred. No. 1.1e+02;
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Pred. No. 1e+02;
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; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER, OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 936
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-936
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9968
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US-10-953-349-9967
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US-10-953-349-9968
                                                                               US-10-953-349-9967
                                                                                                                 CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9967
LENGTH: 538
TYPE: PRT
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ALEXAUROV, Nickolai et al.
APPLICANT: ALEXAUROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9968
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                                                                                                                                                                                                                                                                                                                                                              Sequence 9967, Application US/10953349 Publication No. US20060107345A1
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Best Local Similarity 36.4%;
Matches 12; Conservative
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  Matches
                                       Query Match
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TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                              ORGANISM: Arabidopsis thaliana
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Local Similarity 36.4%;
es 12; Conservative
Local Similarity es 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCRRLLLHESVYDKVLEQLLTSYKQVKIGNP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVYCKQQLLRREVYDFAFRDLCIVYRD---GNP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCRRLLLHESVYDKVLEQLLTSYKQVKIGNP 332
  Conservative
                    36.4%;
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Pred. No. 1.3e+02;
                    Score 55.5; DB 6;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55.5; DB 6;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
  Mismatches
  1.4e+02;
ches 15;
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                                     Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 508;
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  Indels
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; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4398
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US-10-505-928-94
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-94
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US-11-293-697-4398
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Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 866
SOFTWARE: PatentIn 3.2
SEQ ID NO 94
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Best Local Similarity
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/363,019 PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.7%; Score 55.5; DB 7; Length 764; Local Similarity 21.3%; Pred. No. 2e+02;
                                        135 RCMSCCRSSR 144
                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 KFYSKISEYRH-----YCYSVYGTTLEQQYNK-----PLCDLLIRCINXQK 108
                                                                                                                                                                                                     29 ECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                   33;
                                                                                 EE------HKVCRRCDE 903
                                                                                                                                                                 KCTVCK----EGFSLA-RGSCI--PDCEPGTYFDSEL---IRCGECHHTCGTCVGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMESRNLWREVTRYLRLGDIDAATEOKRHLEEKORVEERKRENLRTPW 742
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  NCLSCAGSSR 913
                                                                                                                        EQQYNKPLCDLLIRCINXQK------PLCPE----EKQRHLDKKQRFHNIRGRWTG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVYCKQQLLRREVYDFAFRDLCIVYRD---GNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              6.7%;
nilarity 25.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                              Score 55.5; DB 6; Length 969; Pred. No. 2.6e+02; 9; Mismatches 45; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CPEEKQRHLDKKQRF----HNIRGRW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e+02;
2e+02;
29;
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                                                                                                                                                                                                                                                 43;
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APPLICANT: ALEXANDROV, Nickolai et al.
FITILE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
FITILE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
RUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9684
LENGTH: 433
LENGTH: 433
LENGTH: 433
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US-10-953-349-9684
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US-10-953-349-9685
                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Arabidopsis thaliana US-10-953-349-9684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-10-953-349-9685
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FULE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 4005-2
SOFTWARE: Patentin version 3.3
SEQ ID NO 9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9684, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 KFPGRKYKEHPFWKEKYCPFHEVDG--TPKCCSCER
138 KFPGRKYKEHPFWKEKYCPFHEVDG--TPKCCSCER 171
                                         117 RHLDKKQR------FHNIRGRWTGRCMSCCR 141
                                                                                    106 -KPIAMHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 RHLDKKQR------FHNIRGRWTGRCMSCCR 141
                                                                                                                             57 GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQ 116
                                                                                                                                                                           50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                  2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQL-LRREVYDFAF----RDLCIVYRD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQL-LRREVYDFAF----RDLCIVYRD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKDPVEEDGNLPRVDLNVNHP-HSI----CDGCKSAIEYGRSVHALGVNWHPECFCCRYCD 98
                                                                                                                                                                         FKDPVEEDGNLPRVDLNVNHP-HSI---CDGCKSAIEYGRSVHALGVNWHPECFCCRYCD 105
                                                                                                                                                                                                                                                           6.6%; Score 55; DB 6; Le ilarity 21.8%; Pred. No. 1.2e+02; Conservative 16; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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21.8%;
                                                                                       -FSNTKGRCH
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                            Length 433;
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                                                                                         ITCYERSHPNCHVCKK 137
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RESULT 90
US-11-293-697-3790
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US-11-293-697-3101
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US-11-293-697-3101
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3790
LENGTH: 541
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Matches
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 3101
LENGTH: 541
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                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3790, Application US/11293697 Publication No. US20060105376A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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  495
                                     116 ORHLDKKORFHNIRGRWTGRCMSC 139
                                                                                                                                                           398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 NSHLAVHORLHSREG--PSRCPQC 516
                                                                                                                                                                                               13 POLCTELOTTIHDIILECVYCKOQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSK 72
                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.6%; l Similarity 22.9%; 33; Conservative 1
NSHLAVHORLHSREG--PSRCPQC 516
                                                                                                                                                         PYECKECGKT----FIESAY----LIRHQ------RIHTGEKPYGC-NQCQKLFRN 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRHLDKKQRFHNIRGRWTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAGLIRHQ----RTHTGEKPYECNQCGKAFRDSSCLTKHQRIHTKETPYQCPECGKSFKQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISE-YRHYCYSVYGTTLEQQYNKPLCDLLIR---CINXQKPL-----CPE----EK 115
                                                                                                                   ISE-YRHYCYSVYGTTLEQQYNKPLCDLLIR---CINXQKPL------CPE----EK 115
                                                                           IAGLIRHQ----RTHTGEKPYECNQCGKAFRDSSCLTKHQRIHTKETPYQCPECGKSFKQ 494
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                          6.6%;
                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 55; DB 7; Le
; Pred. No. 1.6e+02;
16; Mismatches 53;
                                                                                                                                                                                                                                       Score 55; DB 7;
Pred. No. 1.6e+02
L6; Mismatches 5:
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RESULT 93
US-11-293-697-3380
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// ORGANISM: Glycine max
US-10-953-349-21080
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 21080
LENGTH: 167
TYPE: PRT
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PAPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9683
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: ENCONDED THERBY
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Local Similarity 21.8%;
10cal Similarity 21.8%;
1es 34; Conservative 16
                                                                                                                                                                                                                                                                                                     / Match 6.6%; Score 54.5; I Local Similarity 20.2%; Pred. No. 50; Local Similarity 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 -KPIAMHE-----FSNTKGRCH------
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                                                                                                                                                               66 CLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQR 124
                                                                                                                                                                                                                                                         14 QLCTELQTTIHDIILECVYCKQQLLR-----REVYDFAFRDLCIVYRDGNPYAVXDK 65
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                                                                                                                     LVKEKERVLEKYNHLFTETGPTKRHKRNS-----FEAKKHVHPTKEKRHQKQSRK 146
                                                                                                                                                                                                               QLC-----H--LMISVYYRNNMLQDLVKLFKGLEAFDRKPRDKSIIQKVANAYEVLG- 96
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Pred. No. 1.6e+02;
L6; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 167;
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Application US/11293697

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, LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3380
                                                                                                                                                                                           US-10-953-349-21078
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21079
LENGTH: 300
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                      Sequence 21078, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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Matches
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               APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Local Similarity 21.2%;
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20.2%; Pred. No. 94;
tive 24; Mismatches
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Pred. No. 88
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                                                                                  FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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                                                                                                    NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33222
LEMETTY ---
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 21078
LENGTH: 308
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Best Local Similarity
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Publication No. US20060107345A1
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Best Local
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
                                                    TYPE: PRT
ORGANISM: Zea mays subsp. mays
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                                                                                              LENGTH: 358
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6.68;
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Pred. No. 1.1e+02;
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Score 54.5;
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US-10-953-349-36844
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33221
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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TYPE: PRT
ORGANISM: Zea mays subsp. mays
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                                                                 347 LPTICSPLRKACTGMDLSAVHDILLKTGYKDDEGAENELSFQEWTQQVQEMLNTKKFGDI 406
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46 AFRDLCIVYRDGNPYAVXDKCLKFYSKI 73
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19; Conservative
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21.6%; Pred. No. 1.6e+02;
tive 15; Mismatches 17;
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5; Mismatches 17;
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NUMBER OF SEQ ID NOS: 40252; SOFTWARE: PatentIn version 3.3; SEQ ID NO 30935; LENGTH: 80; TYPE: PRT; ORGANISM: Triticum aestivum US-10-953-349-30935
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US-10-953-349-30935
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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                                      50 LCIVYR--DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYN
1 MCATORHOGGRPLSEPPRTETSYSHLFFYRHRMYLMFDPTMSLHYN 46
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E7 protein - human papillomavirus type 35
C7.Species: human papillomavirus type 35
A.Note: host Homo Bapins (man)
C7.Species: human papillomavirus type 35
A.Note: host Homo Bapins (man)
C7.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C7.Accession: F40824; S36522
R7.Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A.Title: The phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the phylogenetic relationship and complete nucleotide sequence of human papers of the
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J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10428
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A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus Ela and SV40 larg A;Reference number: S12367; MUID:90107938; PMID:2153075
A;Accession: S12367
                                          R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library,
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C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03688; S12367; T10428
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A; Residues: 1-98 < KEN>
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A;Molecule type: protein
A;Residues: 1-98 <BAR>
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A; Residues: 1-98 < SEE>
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A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Seedorf, K.; Krammer, G.;
Virology 145, 181-185, 1985
A;Title: Human papillomavir
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Best Local :
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        Primer-directed
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    sequencing of human
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Pred. No. 6.2e-50;
0; Mismatches 3
                                              August 1993
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papillomavirus
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R;Cole, S.T.; Streeck, R.E. J. Virol. 58, 991-995, 1986 A;Title: Genome organization A;Reference number: A93020; M

n and nucleotide MUID:86200464; I

PMID:3009902

human

papillomavirus

type

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A;Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers,

GB:M12732; NID:g333049; PIDN:I H.F.J.; Raaphorst, P.M.C.; Mei

A; Molecule type: DNA A; Residues: 1-97 < COL>

A; Accession: A03689

E7 protein - human papillomavirus type 33 C;Species: human papillomavirus type 33 C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 C;Accession: A03689; S23831; S23827

#text_change 09-Jul-2004

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A;Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:9 C;Comment: This protein may be involved in the oncogenic potential of this C;Superfamily; papillomavirus B7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc fing F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T. virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: B32444
A;Accession: B32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B32444
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W7WL31
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A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEL>
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A; Residues: 1-98 <GOL>
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Best Local
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                                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                      69;
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                                                                                                                                                                                          Similarity
                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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CKSTLRLCVQSTQVDIRILQELLMGSFGIVCPNCSTR
                                                                                WRGETPTLQDYVLDLQPEATDLHCYEQLPDSSDEEDVIDSPAGQAEPDTSNYNIVTFCCQ
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73.5%;
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Pred. No. 2.2e-35;
                                                                                                                                                                                        Score 372; DB 1;
Pred. No. 2.5e-34;
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E7 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #te
C;Accession: S36574
R;Dellus; H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human pap
A;Reference number: S36469
A;Accession: S36574
A;Molecule type: DNA
A;Bolariane S36574
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A;Description: HPV type 33 i
A;Reference number: S19906
A;Accession: S23831
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <SNI>
                                                                                                                                                                                    E7 protein - human papillomavirus type 58
C;Specles: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F36779
R;Kirii, Y; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
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S36574
E7 prot
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A;Cross-references: UNIPROT:P36831; UNIPARC:UPI000013841C; EMBL:X74481; NID:g397038; C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
A;Cross-references: UNIPROT:P26557; UNIPARC:UP100000034BB; GB:D90400; NID:g222386; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
                                                              A; Molecule type: DNA
A; Residues: 1-98 < KII
                                                                                                                          A;Title: Human papillomavirus type 58 DNA A;Reference number: A36779; MUID:92024102; A;Accession: F36779
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                                                                  1-98 <KIR>
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57.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 294; DB 2;
Pred. No. 1.2e-25;
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Pred. No. 9.4e-26;
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E7 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A03690
                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-98 <SCH-A,
R;Residues: 1-98 <SCH-A;Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:g60955;
C;Superfamily: papillomavirus E7 protein;
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:g333026; PIDN: C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;58-94/Region: zinc finger CCCC motif
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A;Title: The nucleotide sequence and genome organization
A;Title: The nucleotide sequence and genome organization
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C;Species: human papillomavirus type 6b
C;Date: 30-Sep_1987 #sequence_revision 30
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A; Residues: 1-98 < DAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;59-95/Region: zinc finger CCCC motif
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2341-2348, 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCGTTVRLCINSTTTDVRTLQQLLMGTCTIVCPSCAQQ
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 MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 58
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                                                                         47.0%; ilarity 52.5%; Conservative 1
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                                                                                                                                                                                                                                                                                 and genome organization of genital 90975; MUID:84131949; PMID:6321162
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1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t; Score 245; DB 1; 1; Pred. No. 3.5e-20; 14; Mismatches 29;
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                                                                                             Score 243; DB 1;
Pred. No. 5.9e-20;
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Pred. No. 3.9
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                                                                             28;
                                                                                                            Length 98
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CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97

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E7 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Ate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38503
R;Gstrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RhPV 1 genomic sequence and an int A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: B38503
                   E7 protein - human papillomavirus type 45 C;Species: human papillomavirus type 45 C;Date: 20-Feb-1995 #sequence_revision 20-C;Accession: S36562 R;Delius, H.; Hofmann, B.
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A;Residues: 1-113 <OST>
A;Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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R;Delius, H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus
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A; Residues: 1-97 < DEL>
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E7 protein -
    submitted to the
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;Species: human papillomavirus type 34
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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Best Local Similarity
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H.; Hofmann, B.
to the EMBL Data
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                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDL----QPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAH-----
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                                                                                                                                                                                                           PEDGDCYRIVSDCYSCGKPLRLVVVSSHEELRVLEDLLMGTLDIVCPSCASR 112
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                                                                                                                                                                                                                                                                                           MIGPKPTLEDIVLDLQPFPQPQPVDLMCYEQLSDSSEDEDEVDHHHNNQQQHHQHARPEV
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43.8%; Pred. No. 3.7
Library, August 1993
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Pred. No. 1.1e-17;
18; Mismatches 29;
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                                                            20-Feb-1995 #text_change 09-Jul-2004
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3.7e-17;
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                                                            Query Match
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A;Molecule type: DNA
A;Residues: 1-105 <DEL>
A;Residues: references: UMIPROT:P36832; UNIPARC:UPI000013841D; EMBL:X74482; NID:g397046; PIDN
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
S36528
                                                                                                                                                                                                                                                                                                                                                                                 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August A;Description: Primer-directed sequencing of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 protein - human papillomavirus type C;Species: human papillomavirus type 53 C;Date: 20-Feb-1995 #sequence_revision C;Accession: S36528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P36826; UNIPARC:UPI0000138409; EMBL:X74474; NID:g396973; PID:C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 protein - human papillomavirus type: C;Species: human papillomavirus type 30 C;Date: 20-Feb-1995 #sequence_revision: C;Accession: S36504
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S36504
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A;Rosidues: 1-106 <DEL>
A;Cross-references: UNIPROT:P21736; UNIPARC:UPI0000138416; EMBL:X74479; NID:g397022; PIDPARC:UPI0000138416; EMBL:X74479; NID:g397022; PIDPARC:Uperfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                                                                                                                                                                         A; Reference number: S36469
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A; Accession: S36504
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es 47; Conserv
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sequencing of human
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Score 208.5; DB 2
Pred. No. 4.5e-16;
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Pred. No. 3.5
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of human
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                                    DB 2;
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                                    Length 105;
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Local

Similarity

45;

Conservative

Mismatches

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Gaps

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E7 protein - human papillomavirus type 13
C.Species: human papillomavirus type 13
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: 842955
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; (Virology 190, 587-596, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar A,Reference number: A42955; MUID:92391075; PMID:1325697
A,Accession: B42955
A,Molecule type: DNA
A,Residues: 1-101 <VAN>
A,Residues: 1-101 <VAN>
A,Cross-references: UNIPROT:Q02271; UNIPARC:UPI00001383F9; EMBL:X62843; NID:g60295; PIDN C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;61-97/Region: zinc finger CCCC motif
                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-105 < COL>
A; Residues: 1-105 < COL>
A; Residues: 1-105 < COL>
A; Residues: 1-105 < COL>
C; Superfamily: papillomavirus E7 protein
C; Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                  A;Accession: B26165
A;Molecule type: DNA
A;Residues: 1-105 <SEE>
A;Cross-references: UNIPROT:P06788; UNIPARC:UPI0000000DB5; GB:X04773; NID:g60876;
A;Cross-references: UNIPROT:P06788; UNIPARC:UPI000000DB5; GB:X04773; NID:g60876;
A;Cole, S.T.; Danos, O.
J. Mol. B101. 193, 599-608, 1987
A;Mille: Nucleotide sequence and comparative analysis of the human papillomavirus
A;Reference number: A92937; MUID:87283882; PMID:3039146
A;Accession: H26251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Identification of early proteins of the human papilloma viruses type 16 A,Reference number: A91068; MUID:87218459; PMID:3034571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E7 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text
C;Accession: B26165; R36251
R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp,
EMBO J. 6, 139-144, 1987
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                                            MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTSCSKCCSNVRLVVECTGPDIHDLHDLLLGTLNIVCPLCAPK 100
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  MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.8%;
                                                                                                                 38.8%; Score 200.5;
39.6%; Pred. No. 3.5
                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 200.5; DB 1;
Pred. No. 3.3e-15;
3; Mismatches 35;
                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-Sep-1987 #text_change
                                                                                           3.5e-15;
hes 33;
                                                                                                                                         DB 1;
                                                                                                                                       Length 105;
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                                                                                             Indels
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                                                                                                                                                                                                                                       PIDN: CAA28665.1;
                                                                                           Gaps
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                                                                                                                                                                                                                                          PID:
B44890
E7 protein
C;Species:
                                                                       RESULT
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A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compary A;Reference number: A42955; MUID:92391075; PMID:1325697
A;Recession: B36818
A;Recession: B40818
A;Residues: 1-98 <VAN'>
A;Residues: 1-98 <VAN'>
A;Residues: 1-98 <VAN'>
A;Cross-references: UNIPARC:UDI000013842E; EMBL:X62844; NID:g61010; PIDN:CAA44656.1; PID C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; transforming protein; F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E7 protein - pygmy chimpanzee papillomavirus (type 1)
C;Species: pygmy chimpanzee papillomavirus
C;Date: 30--Unn-1993 #sequence_revision 30--Unn-1993 #text_change 16--Unl-1999
C;Accession: B36818
C;Accession: B36818
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; (Virology 190, 587-596, 1992
                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P27231; UNIPARC:UPI0000138414; GB:M73236
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Human papillomavirus type 42: new sequence, conserved A;Reference number: A39451; MUID:92087479; PMID:1309278 A;Accession: F39451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E7 protein - human papillomavirus type 42 C;Species: human papillomavirus type 42 A;Note: host Homo sapiens (man)
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A; Residues: 1-93 < PHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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Best Local S
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Best Local
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                                                                                                                               1 MHGDTPTLHEYMLDLQP--ET-TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                   MRGETPTLKDIVLFDIPTCETPIDLYCYEQL-DSSDEDD
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CTQCYKSVKLVVQCTEADIRNLQQMLLGTLDIVCPLCAR
                                            CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                        35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.5%; Score 194; DE 46.4%; Pred. No. 1.76 ative 13; Mismatches
                                                                                                                                                                                  17;
                                                                                                                                                                                  Score 183.5; DB 1;
Pred. No. 2.4e-13;
7; Mismatches 27;
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                                                                                                                                                                                                                                 Length
                                                                                            QAKQDIQRYRILCV 52
                                                                                                                                                                                                                                      93;
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18

- human papillomavirus type of human papillomavirus type 66

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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-20 C;Accession: B44890
R;Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type 66 from an invasiv A;Reference number: A44890; MUID:92129556; PMID:1663515
A;Accession: B44890
A;Molecule type: DNA
A;Residues: 1-105 cTAW>
A;Roserence s: UNIFROT:Q80956; UNIPARC:UPI0000138426
A;Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:78639)
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
$15622
E7 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A,Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: $15622
C;Accession: $15622
R;Hirsch-Behnam, A,; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-99, 1990
Virus Res. 18, 81-99, 1990
R; Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August A; Description: Primer-directed sequencing o A; Reference number: $36469 A; Accession: $36580 A; Molecule type: DNA A; Residues: 1-105 < DEL> A; Cross-references: UNIPROT: P36833; UNIPARC
                                                                                                                                                         E7 protein - human papillomavirus type 56 (;Species: human papillomavirus type 56 (;Species: human papillomavirus type 56 (;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 (;Accession: $36580 R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15622
A;Molecule type: DNA
A;Residues: 1-92 <HIR>
A;Residues: 1-92 <HIR>
A;Cross-references: UNIPROT:P22160; UNIPARC:UPI0000138421; EMBL:X55965; NID:g60882; PIDN C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;55-91/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                   RESULT 20
S36580
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34.5%; Score 178.5; DB 1;
Similarity 43.3%; Pred. No. 8.6e-13;
42. Conservative 15; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                         CCKCHSTVRLVVECGAADIRHLEQLFLNTLTIVCPRC
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Pred. No. 2.7e-13;
    UNIPARC: UPI0000138420;
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of human
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  EMBL:X74483; NID:g397053;
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A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_chang
C;Accession: F40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Accession: F40415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P36816; UNIPARC:UPI00001383F3; EMBL:X74463; NID:g397060; C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of hur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $36585
E7 prot
                                                                                                                                                        A;Cross-references: UNIPROT:P26558; UNIPARC:UPI000013841B; GB:M62877 C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-101 < LUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 protein - human papillomavirus type 51 C; Species: human papillomavirus type 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
W7WL51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S36585
R;Delius, H.; Hofman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-111 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                              A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S36585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 protein - human papillomavirus type 7
;Species: human papillomavirus type 7
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
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                                                                                              Local
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45; Conserv
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42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAH-----Y
                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGERPTLGDIVLDLQPEPVS1SCNEQL-DSSDSEDDHE----QDQLDSSHNRQREQPTQ
                                  MHGDTPTLHEYMLDLQPET-TDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH----YNIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDLQVNLQSFKIVTHCVFCHCLVRLVVHCTATDIRQVHQLLMGTLNIVCPNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIHVPCCECKFVVQLDIQSTKEDLRVVQQLLMGALTVTCPLCA 102
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MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE 59
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                                                                                                34.48;
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                                                                          Score 178; DB 1; 1
Pred. No. 1.1e-12;
6; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178.5; DB
Pred. No. 1e-12;
2; Mismatches
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Pred. No. 9.9
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                                                                                                                   Length 101;
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E7 protein - human papillomavirus type 2a (;Species: human papillomavirus type 2a A;Note: host Homo sapiens (man) (pate: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004 C;Accession: $15615
                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-86 <DEL>
A;Residues: NIPROT:P36818; UNIPARC:UPI00001383F6; EMBL:X74465; NID:g396901; PID
A;Crose-references: UNIPROT:P36818; UNIPARC:UPI00001383F6; EMBL:X74465; NID:g396901; PID
C;Superfamily: papillomavirus E7 protein; transcription regulation
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S36533
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A;Residues: 1-92 <HIR>
A;Residues: 1-92 HIR>
A;Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964
A;Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964
C;Superfamily: papillomavirus E7 protein; transcription regulation; zinc
C;Keywords: DNA binding; early protein; transcription regulation; zinc
F;55-91/Region: zinc finger CCCC motif
RESULT 25
336480
236480
E7 protein - human papillomavirus type 17
C;Species: human papillomavirus type 17
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of human A;Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7 protein - human papillomavirus type 10 C;Species: human papillomavirus type 10 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S36533
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Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types
A;Reference number: S15614; MUID:91188699; PMID:1964523
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Best Local S
Matches 40
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Best Local
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                                                                                                                                                                      CSLPLRLVVECSHADIRALEQLLLGTLKLVCPRC
                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                                                    WHGPHPTVKDIELSLAPEDIPV-----CNVQLDEEDYTDA----VEPAQQAYRVVTECTK
                                                                                                                                                                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                       33.6%; Score 173.5; 42.6%; Pred. No. 2.
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13; Mismatches
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                     #text_change 09-Jul-2004
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36480
A;Accession: S36480
A;Molecule type: DNA
A;Residues: 1-95 <DEL>
A;Cross-references: UNIDROT:D36821; UNIDARC:UDIO0001383FB; EMBL:X74469; l
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Volpers, C.; Streeck, R.E. Virology 181, 419-423, 1991
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: B38502
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E7 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38502
A;Molecule type: DNA
A;Residues: 1-104 <DEL>
A;Residues: 1-104 <DEL>
A;Cross-references: UNIPROT:P36827; UNIPARC:UPI000013840B; EMBL:X74475;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                     E7 protein - human papillomavirus type 32 (;Species: human papillomavirus type 32 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S36510 R;Dellus, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                           RESULT
S36510
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                                                                                                                           A; Reference number: S36469
A; Accession: S36510
                                                                                                                                                                        submitted to the EMBL Data Library, August A;Description: Primer-directed sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-109 < VOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRGPKPTLQEIVLDLCPYNBIQPVDLVCHEQLGES---BDBIDBPDHAVNHQHQLLARRD
                                                                                                                                                                                                                                                                                                                                                                                                                                             EPOR--HTIQCSCCKCNNTLQLVVEASRDTLRQLQQLFMDSLGFVCPWCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 170; DB
Pred. No. 9.1e-
16; Mismatches
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                                                                                                                                                                             papillomavirus types
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                                                       NID: g396981;
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C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: D40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Ritle: Characterization of a novel human papillomavirus DNA in the cervical A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: D40509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E7 protein - human papillomavirus type 27
C;Species: human papillomavirus type 27
C;Species: human papillomavirus type 27
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36498
R;Delius, H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
                                                                                                                                                                                                                                                            A;Residues: 1-110 <REU's A;Residues: 1-110 <REU's A;Cross-references: UNIPROT:P27963; UNIPARC:UPI000013842B; GB:M73258; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation
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A; Residues: 1-92 < DEL>
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Best Local (
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                                                                                                                                                                            36;
                                                                                                                                                                                              Similarity
QRHTIQCTCCKCNNLLQLVVEASRENLRNVELLFMDSLNFVCPWCA
                                                                                                                                MHGDTPTLHEYMLDLQP----ETTDLYXYXQLNDSSEEEDEIDGPAGQAE-----PDR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQ--PETTDLYXYXQLNDSSEEED--EIDGPAGQAEPDRAHYNIVT
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                                         AHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                    MHGPKPTVQEIVLELCPCNEIEPVDLVCHEQLGDSDDEIDEPDHAVNHHQHQLLARRDEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHGTRPSLADITLILEEIPEIIDLHCDEQF-DSSEEENNHQLTEPAVQA-----YGVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRGNAPTLKDIILYDLPTCDPTTCDTPPVDLYCYEQFDTSDEDDEDDDQPIKQ---DIQR 57
                                                                                                                                                                            Conservative
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39.4%;
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                                                                                                                                                                            20;
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                                                                                                                                                                                              Score 157.5; DB 1; Pred. No. 2.3e-10;
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Pred. No. 1.1e-11;
                                                                                                                                                                            Mismatches
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tches 32;
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C;Accession: S36545
C;Accession: S36545
R;Delius, H.; Hofmann, B.
R;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
Submitted to the EMBL Data Library, August 1993
                                                                                                                              E7 protein - human papillomavirus type ? C;Species: human papillomavirus type 26 C;Date: 20-Feb-1995 #sequence_revision ?
                                                                                                                                                                                                          RESULT
S36545
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A;Residues: 1-93 <DEL>
A;Residues: 1-93 <DEL>
A;Crose-references: UNIPROT:P36820; UNIPARC:UPI00001383FA; EMBL:X74468; NID:g396924;
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the EMBL Jacobs decreased of hu
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A;Residues: 1-111 <DEL>
A;Residues: 1-111 <DEL>
A;Cross-references: UNIPROT:P36829; UNIPARC:UPI0000138412; EMBL:X74478; NID:g397014; PID:
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 protein - human papillomavirus type 15
C;Species: human papillomavirus type 15
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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S36474
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A; Accession: S36474
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                        A; Reference number: S36469
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A; Accession:
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S36545
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                                                                                                                                                                                                                                                                                                    CFCDSKLRLIVVATPFGIRSQQDLLLEEVKLVCPGCREK
                                                                                                                                                                                                                                                                                                                                                  CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDLQVNLQSFKVVTRCVFCQCLVRLAVHCSITDITQFQQLLMGTLHIVCPNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHGERPTLGDIVLNLHPEPVCLNCNEQL-DSSDSEDDHE----QDQLDSLHSREREQPTQ
                                                                                                                                                                                                                                                                                                                                                                                                   MIGKEATIPDIVLELQELVQPTDLHCYEEL---SEEETE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 150.5; DB: 35.4%; Pred. No. 1.4e-09 tive 14; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148; DB 2;
Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                          20-Feb-1995
                                              of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                      #text_change 09-Jul-2004
                                              papillomavirus types.
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                                                                                                                                                                                                                                                                                                         89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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E7 protein - human papillomavirus type la
C;Species: human papillomavirus type la
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C17475
R;Danos, O.; Katinka, M.; Yaniv, M.
EMBO J. 1, 231-236, 1982
A;Title: Human papillomavirus la complete DNA sequence: a novel type of genome organizat
A;Reference number: A90970; MUID:84182467; PMID:6325156
A;Accession: C17475
A;Accession: C17475
A;Rolecule type: DNA
A;Residues: 1-93 cDAN'
A;Cross-references: UNIPROT:P06465; UNIPARC:UPT00001383FD; GB:V01116; GB:X03321; NID:g66
R;Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A;Title: Comparative analysis of the human type la and bovine type 1 papillomavirus gend
A;Reference number: A92993; MUID:83189357; PMID:6302319
C;Superfamily: papillomavirus E7 protein
C;Superfamily: papillomavirus E7 protein
                                                                                                                  R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing o
A;Reference number: S36469
A;Accession: S36591
A;Molecule type: DNA
A;Residues: 1-93 <DEL>
                                                                                                                                                                                                                                            B7 protein - human papillomavirus type 9
(;Species: human papillomavirus type 9
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36591
R;Dellus, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                    RESULT 34
S36591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-104 <DEL>
A;Residues: 1-104 <DEL>
A;Crose-references: UNIPROT:p36824; UNIPARC:UPI0000138404; EMBL:X74472; NID:g396956;
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
                                                     A;Cross-references: UNIPROT:P36817; UNIPARC:UPI00001383F5; EMBL:X74464; NID:g397068; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WHGDTPTLHEYMLDLQPB-TTDLYXYXQLN----DSSEEEDBIDG------PAGQAEPD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVGEMPALKDLVLQLEPSVLDLDLYCYEEVPPDDIEEELVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGNIINIEDVILDLVPQPEIDLRCYEQLDYEQFDSS-DEDETDNWRDQQARQAGQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 138; DB 1; 33.0%; Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.2%; Score 140.5; 36.4%; Pred. No. 1.7
23.6%;
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Score 122; DB 2;
Pred. No. 1.7e-06;
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                                                                                                                                                                                                        c 1993
of human
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                                                                                                                                                                                                        papillomavirus
                   Length 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 104;
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836539
E7 protein - human papillomavirus type 12
C;Species: human papillomavirus type 12
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: $36539
                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-103 <DEL>
A;Residues: 1-103 <DEL>
A;Cross-references: UNIPROT:P36819; UNIPARC:UPI00001383F8; EMBL::C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                     R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer_directed sequencing of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P36823; UNIPARC:UPI0000138403; EMBL:X74471; NID:g396948; PID:
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S36492
R;Dellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 35

336492

E7 protein - human papillomavirus type 25

C;Species: human papillomavirus type 25

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995

C;Accession: S36492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-102 < DEL>
                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S36539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S36469
                                                                                                                                                                         Matches
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                                                                                                                                                                                                               Query Match
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35; Conservative
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                                                                                                                            1 MHGDTPTLHEYML---DLQPET--TDLYXYXQLNDSSEEEDEIDGPAGQABPDRAHYNIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHGDTPTLHEYML---DLQPET--TDLYXYXQLNDSSEEBDEIDGPAGQAEP--DRAHYN 53
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                                                                                                                                                                                           Similarity
                                     T--FCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC
                                                                                    MIGKEVTVQDFTLELSELQPEVLPVDLLCEEELPNEQETEEESD-
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APCGCSSCEVNLRIFVNATDTGIRTLQDLLISDLQLLCPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVAPCGCCEVKLRIFVKATDFGIRTLQNLLIEELQLLCPEC
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                                                                                                                                                                    Conservative
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Pred. No. 2.8e
17; Mismatches
                                                                                                                                                                    Score 119; DB 2;
Pred. No. 4.1e-06;
6; Mismatches 37
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ches 34;
                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                               Length 103
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                                                                                    IDRTVFKII
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37

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E7 protein - human papillomavirus type 5
(;Species: human papillomavirus type 5
(;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
(;Accession: G26277
(;Accession: G26277
(;Accession: G26277
(;Title: Nucleotide sequence and genome organization of human papillomaviru: A;Title: Nucleotide sequence and genome organization of human papillomaviru: A;Reference number: A94360; MUID:87207670; PMID:3033892
A;Accession: G26277
A;Molecule type: DNA
A;Residues: 1-103 <ZAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-103 <KIY>
A;Crose-references: UNIPROT:P22423; UNIPARC:UPI0000138417; GB:M32305; NID:g333062;
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
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A;Cross-references: UNIPROT:P36822; UNIPARC:UPI00001383FC; EMBL:X74470; NID:g396940; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding: APT'V TYPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 protein - human papillomavirus type 19
C;Species: human papillomavirus type 19
C;Adte: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36486
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Bescription: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kiyono, T.; Adachi, A.; Ishibashi, M. Virology 177, 401-405, 1990 A;Title: Genome organization and taxonomic A;Reference number: A35324; MUID:90281611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: host Homo sapiens (man)
G;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: B35224
R;Kiyono, T.; Adachi, A.; Ishibashi, M.
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Matches 33
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                                                                                                                                                                                                                                                                                                                                                                                         TFC-CK-CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIGKEVTVRDIVLELSEVQPEVLPVDLFCDEELPNEQQAEEELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDL---QPET--TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVVLCGCCKVKLRIFVKATQFGIRTLQDILIEELQLLCPEC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 1; Length 103; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  position of human papillomavirus type PMID:2162112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5; DB 2;
7.8e-06;
ches 35;
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A;Cross-refe
C;Superfamil
C;Keywords:
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J. Virol. 58, 626-634, 1986
A; Title: Epidermodysplasia verruciformis-associated human papillomavirus
A; Reference number: A93019; MUID:86200410; PMID:3009874
A; Accession: A03691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: F40480
R;Yabe, Y.; Sakai, A.; Hitsumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A;Title: A subtype of human papillomavirus 5 (HPV-5b) and A;Reference number: A40480; MUID:91306467; PMID:1649510
A;Accession: F40480
A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
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A;Residues: 1-103 <YAB>
A;Cross-references: UNIPROT:P26559; UNIPARC:UPI00000006C7; GB:D90252;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                A;Cross-references: UNIPROT:P06430; UNIPARC:UPI00001383F4; A;Note: this ORF is not annotated in GenBank entry PPH8CG
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C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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                                                                                                                                           ;Superfamily: papillomavirus E7 protein;Keywords: DNA binding; early protein; t
                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                    Accession: A03691
                                                                                                                                                                                                                                                                                                                                                                                  7 protein - human papillomavirus type 8
;Species: human papillomavirus type 8
;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
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                                                               l Similarity
33; Conserv
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32; Conservative
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                                                                 Conservative
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                                                                                                                                           early protein; transcription regulation
                                                                             20.3%;
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31.7%; Pred. No. 5.4e-05;
... Mismatches 37;
                                                               17;
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Pred. No. 2.5e-05;
8; Mismatches 37;
                                                             Score 105; DB 1; 1
Pred. No. 0.00015;
7; Mismatches 37;
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E/ protein - cottontail rabbit papillomavirus
C:Species: cottontail rabbit papillomavirus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Feb-1997
C;Accession: A03692
R;Giri, I; Danos, O.: Yaniv M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    early protein E7 - bovine papillomavirus type 4
C;Species: bovine papillomavirus type 4
C;Species: bovine papillomavirus type 4
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: B61399
C;Accession: B61399
R;Jackson, M.B.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindlay, G.J.; Campo, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Giri, I.; Danos, O.; Yaniv, M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope) papil
A;Reference number: A94027; MUID:85166175; PMID:2984661
A;Accession: A03692
A;Accession: A03692
A;Molecule type: DNA
A;Residues: 1-94 <GIR>
A;Cross-references: UNIPARC:UPI000000954
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein;
RESULT 44
$19907
E7-C protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: $19907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Carcinog. 4, 382-387, 1991
A;Title: The B subgroup bovine papillomaviruses lack an A;Reference number: A61399; MUID:92000191; PMID:1654923
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q7LZV7; UNIPARC:UPI000002F8BF; GB:X59063C;Superfamily: bovine papillomavirus type 4 E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-98 < JAC>
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEE---DEIDGPAGQAEPDRAHYNIVTF 57
                                                                                                                                                                                                                                                                                                                                                               27;
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                                                                                                                                                                                                                            CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLR-LCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFC-CK-CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC
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                                                                                                                                                                               CYACEQVEREAVVTSTEGIHQEQQLEFDNEFLECAACSKQ
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                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                                                                                             Score 83.5; DB 2; Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                               40; Indels
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                         09-Jul-2004
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C;Species: deer papillomavirus
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_ch
C;Date: 28-May-1996 #sequence_revision 28-May-1986 #text_ch
C;Accession: A03593
R;Groff, D.E.; Lancaster, W.D.
J. Virol. 56, 85-91, 1985
A;Title: Molecular cloning and nucleotide sequence of deer
A;Reference number: A93013; MUID:85293253; PMID:2993669
A;Accession: A03693
                                                                       A;Molecule type: DNA
A;Residues: 1-102 <GRO>
A;Cross-references: UNIPARC:UPI000017495D
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; t:
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A;Cross-references: UNIPROT:Q8BDD8; UNIPARC:UPI00000FA386; GB:X59062
C;Superfamily: bovine papillomavirus type 4 E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindlay, G.J.; Campo, M.S. Mol. Carcinog. 4, 382-387, 1991
A;Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading fran A;Reference number: A61399, MUID:92000191; PMID:1654923
A;Accession: A61399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     early protein E7 - bovine papillomavirus type 3
C;Species: bovine papillomavirus type 3
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A61399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q81886; UNIPARC:UPI00000F593F; EMBL:X64086; NID:g60282; C;Superfamily: papillomavirus E7 protein C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via A;Reference number: $19906
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A; Residues: 1-55 < SNI>
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 46
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A;Molecule type: DNA
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15.0%;
llarity 32.3%;
Conservative
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                                                                              early protein; transcription
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Score 77.5; DB Pred. No. 0.17; B; Mismatches
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Pred. No. 0.047;
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                                       DB 1;
  31,
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38

IDGPAGQAEP--DRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS

95

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E7 protein - human papillomavirus type 49
C;Species: human papillomavirus type 49
C;Species: human papillomavirus type 49
C;Accession: $36568
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Reference number: $36469
A;Accession: $36568
A;Accession: $36568
A;Accession: $36568
A;Accession: $36469
  RESULT 49
W7WLEP
E7 proteir
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c;Species: human papillomavirus type 41
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: B43550
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C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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C;Keywordes DNA binding; early protein; transcription regulation; transforming prote E;62-99/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Nucleotide sequence of A;Reference number: A43550 A;Accession: B43550
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European
                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQ-PETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH---YNIVT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQ---PETTDLYXXXQLNDSSEEEDEIDGPAGQA-EPDRAHYNIVT 56
                                                                                                     TCGGGCGARLRVFVLATDAAIRSFQELLLEELQFLCPQCREE
                                                                                                                                           FC-CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                     MIGKEVTIPDIILQEEFGQPIDLQCYENLTAEAPAEQEL----EAEEELIQGIPYKVIA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCCKCDSTLRLCVQSTHVDIRTLEDLLMGT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCPFCQAIIRFVCVASNTGIRNLQALLVNS
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                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
    e1k
                                                                                                                                                                                                                                                                                    14.5%;
papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.7%; Score 76; DB 1;
26.7%; Pred. No. 0.29;
tive 17; Mismatches 49
                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                               Score 75; DB 2; Length 103; Pred. No. 0.33; Indels 21; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          papillomavirus
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                                                                                                                                                                                                                                                                 10;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C99767
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96767
A;Accession: C96767
A;Accession: C96767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-102 <PET>
A;Residues: 1-102 <PET>
A;Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:AAA66850.1; PID:gC;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: European elk papillomavirus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B29499; G94457; G94506
R;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
Gene 50, 195-205, 1986
A;Title: Organization and expression of the transforming region from the Eu
A;Reference number: A91567; MUID:87219878; PMID:3034730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Pettersson, U.
submitted to GenBank, August 1987
A;Reference number: A94506
A;Accession: G94506
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A;Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:AAA66850.1; PID:g
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A; Accession: G94457
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A; Residues: 1-102 < AHO>
                                                                                                                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                             A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B29499
                                                                                                                                                                                                                                                                                                                                                                    ;Cross-references:
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                          Similarity
--NIVTFCCKCDSTLRLCVQSTHVDIRTLED
                                                                              LHAENLGIESVLVDGEPTVFEYYPHHÓNSETESNWNSVSDPÁSAÁDAAAMEYVGVLKRED 118
                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGQAEPDRAH---YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                                                                                                                                                                    UNIPROT: Q9C9B7; UNIPARC: UPI00000A4ABB; GB: AE005173; NID: g7109476;
                                                                                                                                                                                                          13.6%;
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                                                                                                                                                                                  Score 70.5; D
Pred. No. 16;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73.5; DB Pred. No. 0.48;
                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                     Length 1273;
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                                                                                                                                    52
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                                                                                                                                                                                     <u>ب</u>
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Marziali,
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submitted to the EMBL Data Library, September 1993
A;Reference number: $37431
A;Reference number: $37431
A;Reference number: $37431
A;Reference preliminary
A;Molecule type: mRNA
A;Residues: 1-3924 <CHA>
A;Residues: 1-3924 <CHA>
A;Cross-references: UNIPROT:Q01484; UNIPARC:UPI0000125B19; EMBL:Z26634; NID:g406287; PIC
A;Ctos E; Kunimoto, M; McLaughlin, T; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A;Reference number: A39643; MUID:91302466; PMID:1830053
A;Accession: A39643
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S37431
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submitted to the EMBL Data Library,
A;Description: The murine rck gene e
A;Reference number: $24241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G;Species: Mus musculus (house mouse)
G;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
G;Accession: 14873; S24241
R;Bladt, F.; Birchmeier, C.
Bifferentiation 53, 115-122, 1993
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C;Species: M:--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ankyrin 2, neuronal long splice form - human
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-622 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Characterization and expression analysis of the murine rck gene: a protein A;Reference number: I48733; MUID:93366030; PMID:8359591
A;Accession: I48733
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                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2077 <OT1>
A;Cross-references: UNIPARC:UPI0000177547; GB:X56957
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPARC:UPI000002747F; EMBL:X66983; NID:g53913; PIDN:CAA47392.1; PID
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ilarity 32.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 2;
Pred. No. 14;
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                                                  R; Pearson, D.; Churcher, C
submitted to the EMBL Data
A; Reference number: Z21774
                                                                                                                                    short-chain dehydrogenase/reductase (EC 1.-.-.) SPAC22A12.17c [similarity] -
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 05-Oct-2004
C;Accession: T38157
A; Accession: T38157
A; Molecule type: DN
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1-261 <PEA>

Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, ne EMBL Data Library, September 1997

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Data Library, September

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A;Title: 440-kD ankyrinB: structure of the major developmentally regulated A;Reference number: A49462; MUID:94075409; PMID:8253844

A;Accession: A49462

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-3924 <RES>
A;Cross-references: UNIPARC:UPI0000125B19; EMBL:Z26634; NID:g406287; PIDN:CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:127607; OMIM:106410
A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status |
                                                                                                                                        F;727-759/Domain: F;760-792/Domain: F;793-825/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chan, W.; Kordeli, E.; Bennett, V
J. Cell Biol. 123, 1463-1473, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000016A55B; GB:M37123; NID:g178647; PIDN:AAA62828.1; R;Chan, W.; Kordeli, E.; Bennett, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 463-474, 'PE', 477-495 <TSE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Tse, W.T.; Menninger, J.(
Genomics 10, 858-866, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                               F;191-223/Domain:
F;232-264/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
                                                                                                                                                                                                                                  F;628-660/Domain:
                                                                                                                                                                                                                                                                  F;562-594/Domain:
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                                                                                                                                                                                                              661-693/Domain:
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                                 DTPTLHEYMLDLQPETTDLYX--YXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVT 56
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Pred. No. 1e+0
L5; Mismatches
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                                                                                      DB 2;
le+02;
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E6 protein - bovine papillomavirus type 4
C;Species: bovine papillomavirus type 4
C;Species: bovine papillomavirus type 4
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #tc
C;Accession: B27129
R;Patel, K.R.; Smith, K.T.; Campo, M.S.
J. Gen. Virol. 68, 2117-2128, 1987
A;Title: The nucleotide sequence and genome organizati
A;Reterence number: A92795; MUID:87282264; PMID:303904
A;Accession: B27129
A;Molecule type: DNA
A;Residues: 1-99 <ATT>
A;Residues: 1-99 <ATT>
C;Superfamily: bovine papillomavirus type 4 E6 proteir
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: ABO502; MUID:21534947; PMID:11677608
A;Accession: AD0782
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C;Superfamily: microbial L-serine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaoxa, P.
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C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
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A; Residues: 1-455 < PAR>
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Pred. No. 19;
       UNIPARC:UPI00001383AE;
s type 4 E6 protein
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PMID:3039043
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R:HByasui, N.; Yasunaga, T.; Kuhara, S.; Suzzz, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Suzzz, DNA Res. 8, 11-22, 2001

DNA Res. 8, 11-22, 2001

A, Title: Complete genome sequence of enterohemorrhagic Escherichia
A, Title: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                     hypothetical protein ydbD [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Capecies: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: H85738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8X9S0; UNIPARC:UPI00000D07B3; GB:BA000007; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
A;Gene: ECs2009
                                                                                                               A;Cross-references: UNIPROT:Q8X9S0; UNIPARC:UPI00000D07B3; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-770 <STO>
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                                                                                                                                                                                                                                                           iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                              R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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Matches
                       Query Match
Best Local
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N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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   Similarity
17; Conser
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGQLLRMTPQESDKIAVYLYQKF---
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     Conservative
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                       12.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
 Score 65; DB;
Pred. No. 38;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Shiba, T.; Hattori,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.; Ishii, K.; Yokoyama,
; Hattori, M.; Shinagawa,
   20;
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                                    Length
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   Indels
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                                                                                                                                GB:AE005174; NID:g12515309;
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     16;
                                                                                                                                                                                                                                                                                J.D.; Rose,
Potamousis,
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K.; Ag
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HEYMLDLQPETTD----LYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVT-------

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C;Accession: D86342
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Raithors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: D86342
A; Accession: D86342
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A;Residues: 1-100 <JAC>
A;Residues: 1-100 <JAC>
A;Cross-references: UNIPROT:Q7LZV6; UNIPARC:UPI0000178418; GB:X59064
C;Superfamily: bovine papillomavirus type 4 E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Carcinog. 4, 382-387, 1991
A;Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading A;Reference number: A61399; MUID:92000191; PMID:1654923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          early protein E7 - bovine papillomavirus type 6
C;Species: bovine papillomavirus type 6
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: C61399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                           A; Map position:
C; Superfamily: 1
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C;Genetics:
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A; Residues: 1-614 <STO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F9H16.6 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D86342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: C61399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                Similarity
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VTFCCKCDSTLRLCVQSTHV--DIRTLEDLLMGTLGIVXPICSQ 96
                                                  PAIHPAMVDLKGKAYDL-----LRQNAQKFLMEDLYRNPGPLQYDGPGADAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C----CK-CDSTLRLCVQSTHVDIRTLEDLLM-GTLGIVXPICSQK 97
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                                                                                                  PTLHEYMLDLQPETTDLYXYXQLNDSSEE---ED----EIDGPAGQAEPDRAHYNI
                                                                                                                                                                                                                                                        pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructok
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                   UNIPARC: UPI000004829A; GB: AE005172; NID: g4836893; PIDN: AAD30596.1;
                                                                                                                                                                             12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 64.5;
26.2%; Pred. No. 4.
                                                                                                                                                     15; Mismatches
                                                                                                                                                                             Score 64.5;
Pred. No. 34
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Mismatches
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                                                                                                                                                                                                     DB 2;
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                                                                                                                                                  28; Indels
                                                                                                                                                                                                   Length 614;
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                          A;Cross-references: UNIPROT:Q39436; UNIPARC:UPI00000AD016;
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C; Superfamily: Phospholipase A2
C; Superfamily: Phospholipase A2
C; Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-38/Domain: propeptide #status predicted <PRO>
F;17-38/Domain: propeptide #status predicted <PRO>
F;39-76,84-118,125-138/Product: crotcoxin acidic subunit that status experimental <CHA>
F;39-76/Domain: crotoxin acidic subunit chain B #status experimental <CHB>
F;18-118/Domain: crotoxin acidic subunit chain C #status experimental <CHC>
F;125-138/Domain: crotoxin acidic subunit chain C #status experimental <CHC>
F;42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F;43,45,47,64/Bainding site: calcium (Tyr. Gly. Asp) #status predicted
F;44/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental e
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14580
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Biochemistry 24, 7054-7058, 1985
A;Title: Rattlesnake presynaptic neurotoxins: primary structure and evolutionary origin A;Reference number: A90500; MUID:86104201; PMID:4084559
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A;Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.
A;Reference number: S01392; MUID:89016587; PMID:3174444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phospholipase A2 homolog crotoxin acidic subunit precursor - tropical rattlesnake C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel) C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 16-Aug-2004 C;Accession: S01392; A23861; S11382; B23861; C23861
                                                                                                                                                                                                                                        R;Alexandrova, R.; Barkla, B.; Blumwald, submitted to the EMBL Data Library, June A;Reference number: Z18149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 'Z',85-118 <AIR2>
A;Cross-references: UNIPARC:UPI000017277A
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A; Residues: 1-138 <BOU>
                                                                                                                                                                                             A; Accession: T14580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIEP1L protein precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S01392
                                           A; Residues: 1-391 < ALE>
                                                                                      A; Molecule type: mRNA
                                                                                                                                 A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AVSLCVEDQDYMGRIKKLQEYLDQVRTIVKPGCSQ 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTDVYTYRQ-----EDGEIVCGEDDPCG-----
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                                                                                                                                                 from GB/EMBL/DDBJ
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1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQICECDKAAAICFRNS 115
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EMBL: X87931; NID: g1107525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: X12606; NID: g62685; PIDN
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bae

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A;Pitle: Studies of the sequence of Mojave toxin: the acidic subunit.

A;Reference number: A38106

A;Accession: A2Accession: Acceptance accidic subunit Acceptance accidiced

A;Accession: A2Acceptance accidiced

A;Acceptance A2Acceptance accidiced

A;Acceptance A2Acceptance accidiced

A;Acceptance A2Acceptance accidiced

A;Acceptance A2Acceptance accidiced

A;Acceptance A2A
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A;Accession: A33006
A;Accession: protein
A;Molecule type: protein
A;Residues: 41-80;84-119;127-138 <BIE>
A;Residues: 41-80;84-119;127-138 <BIE>
A;Cross-references: UNIPARC:UPI000017277B; UNIPARC:UPI000017277C; UNIPARC:UPI000017277D
R;Bieber, A.L.; Becker, R.R.; McParland, R.; Hunt, D.F.; Shabanowitz, J.; Yates III, J.F.
Toxicon 27, 31, 1989
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A;Title: Genomic sequences encoding the acidic and basic A;Reference number: I51380; MUID:94156205; PMID:8112610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Crotalus scutulatus scutulatus (Mojave rattlesnake)
C;Date: 13-Sep-1996 #sequence revision 14-Feb-1997 #text_change 16-Aug-2004
C;Accession: I51380; A33006; A38106
R;John, T.R.; Smith, L.A.; Kaiser, I.I.
Gene 139, 229-234, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P18998; UNIPARC:UP10000131109; EMBL:U01026; NID:g451315; R;Bieber, A.L.; Becker, R.R.; McParland, R.; Hunt, D.F.; Shabanowitz, J.; Yates III, submitted to the Protein Sequence Database, November 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: siepll
C;Superfamily: S-locus glycoprotein; S-locus-specific glycoprotein homology
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-391/Product: SIEP1L protein #status predicted <MAT>
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A; Residues: 1-138 < JOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospholipase A2 homolog Mojave toxin acidic subunit precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
       19 TTDLYXYXQLNDSSEEEDEI----DGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLYFSMLDLSKSSLKEVTFSCSPENDDNYAY----DITFAYQSIDGSIGGNAEIARPKY 276
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<del>..</del>
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                                                                                                                                         Score 63; DB 1; Length 138; Pred. No. 9.9;
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Pred. No. 27;
                                                                                                            Mismatches
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C; Keywords: ATP
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Best Local :
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A; Residues: 1-1250 < LYN>
A; Cross-references: UNIPROT: 094385; UNIPARC: UPI000006C88E;
A; Cross-references: Strain 972h-; cosmid c29A10
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T40062
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, submitted to the EMBL Data Library, December 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable nuclear envelope pore membrane protein - fission yeast (Schizosacc C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: 221903
A; Accession: T40062
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A;Residues: 1-586,'KCFKNHST',595,'TCLQC',601,'KHFEN',607-855 <KRO>
A;Cross-references: UNIPARC:UPI00001689F1; EMBL:U15300; NID:g557483; PIDN:AAA50395.1;
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C;Species: Saccharomyces cerevisi
                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, submitted to the Protein Sequence Database, Septem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              맑
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A;Residues: 1-855 <OBE>
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;509-517/Region: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                  SPDB:SPBC29A10.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 SNKQEDSDDTEGKAGTTNDDTSHKPCSQKYGKSIGVVGAGAYGVVKICARCKTAKDVLPY 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                   Similarity
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IHNSSRILGOYTLQVLPEGTAKINPLHENYCLNSLRKDQ-
                                          MHGDTPTLHEYMLDLQPETT----DLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTDVYTYRQ-----EDGEIVCGGDDPCG------TQICECDKAAAICFRDS 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%;
                                                                                                                 12.2%; Score 63; DB 2;
22.8%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ibrary, September 1994
cerevisiae HALS gene,
                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 2;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                             GB/EMBL/DDBJ
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                                                                                                                                       Length 1250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 855
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                                                                                                                                                                                                                                                                                         EMBL:AL034463; PIDN:CAA22435.J
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  --YVD
                                                                                          Gaps
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  182
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RESULT 66
T00198
                    hypothetical protein F8F16.240 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04509 R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.: Scharfe, M.: Schon O. Wahad.
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A;Gene: vp80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Jin, T.; Qi, B.; Qi, Y.
submitted to the EMBL Data Library, December 1997
A;Description: Leucania separata multiple nuclear polyhedrosis virus genome DNA 5118bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 23-A;
C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:F02E9.4
A;Map position: 1
A;Introns: 225/3; 321/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1996
A;Reference number: Z19285
A;Accession: T20513
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1490 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F02E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-675 <JIN>
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A; Accession: T00198
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A;Cross-references: UNIPROT:O01319; UNIPARC:UPI000007CA61; EMBL:281494; PIDN:CAB04052.1
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;Species: Leucania separata nuclear polyhedrosis virus
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
;Accession: T00198
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Best Local (
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M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon,
d to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1385 DDEEDEDDEEDGPSGADEPESTSGSGNVPMDHLNI 1419
                                                                                                                                                                                                                                                                                                      436 VEGNEPTLG-----RPMSRQRYIDTQLIG-----DGGSFEPPPDQAQHPVVEALLN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 NDSSEEEDEIDGPAGQAEPDRA-----HYNI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                   1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                ----CDSTLRLCVQSTHVDIRTLEDL 82
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%; Score 62; DB 25.6%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.1%; Score 62.5; DB 2; Length 1490;
37.1%; Pred. No. 1.5e+02;
tive 5; Mismatches 8; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
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                          O.; Hoheisel,
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                      A; Reference number: A; Accession: T21104
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  A;Status: preliminary; translated
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Ryfheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
hypothetical protein F19B2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T21104 R;Mortimore, B. submitted to the EMBL Data Library, January 1998 A;Reference number: Z19374
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A;Accession: T04509
A;Molecule type: DNA
A;Residues: 1-433 <BEV>
A;Cross-references: UNIPROT:O49591; UNIPARC:UPI00000AB12F;
A;Experimental source: cultivar Columbia; BAC clone F8F16
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 14/1; 57/3; 246/3; 303/2; 394/3
A; Note: F8F16.240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-508 <STO>
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                                                                                                                                                                       T21104
                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
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                                                                                                                                                                                                                                                                    261 VHYCCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stein, 73879-71181 [imported] - Arabidopsis thaliana
Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                64 TLRLCV 69
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                                                                                                                                                                                                                                                                                                                                                                                                           6 PTLHEYMLDLQPETTDLYXYXQLNDSSEE--EDEIDGPAGQAEPDRAHYNIVTFCCKCDS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 59;
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Pred. No. 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE005172; NID:g10645505;
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Z

#sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

from GB/EMBL/DDBJ

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endo-1,3(4)-beta-glucanase (EC 3.2.1.6) 1, Osg1 - rice
N;Alternate names: endo-1,3(4)-beta-glucanase; endo-1,3-beta-glucanase; Osg1 F.
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: O9-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C;Accession: JC7867
R;Yamaguchi, T.; Nakayama, K.; Hayashi, T.; Tanaka, Y.; Koike, S.
Biosci. Biotechnol. Biochem. 66, 1403-1406, 2002
A;Ritle: Molecular cloning and characterization of a novel beta-1,3-glucanase A;Reference number: JC7867; MUID:22152203; PMID:12162569
A;Accession: JC7867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonmuscle myosin II heavy chain A - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59282
R;Bhati.Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
Mech. Dev, 78, 33-36, 1998
A;Title: Differential expression of non-muscle myosin heavy chain genes duri A;Reference number: A59282; MUID:99077683; PMID:9838676
A;Accession: A59282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-823 <WIL>
A;Cross-references: UNIPROT:Q9XXS6; UNIPARC:UPI0000060FA9; EMBL:AL021447; NID:e1519050;
A;Experimental source: clone F19B2
C;Genetics:
                                                                                                                                                  A;Cross-references: UNIPROT:Q8LP99; UNIPARC:UPI00000A0FDD; DDBJ:AB070742
C;Comment: This enzyme, a hydrolytic enzyme, which belongs to monocotyledonous endo-beta
glucans, synergistically acts with chitinase to inhibit fungal growth in vitro. It is al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-1964 <BHA>
A;Cross-references: UNIPROT:093522; UNIPARC:UPI00000FB8F7; GB:AF055895; NID:g3660671; PI
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-338 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: cell line XTC
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;84-764/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
A59282
                             A; Introns: 2
C; Keywords:
                                                                          C;Genetics:
A;Gene: osgl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1053 LEGDSTDLHDQIAELQAQIAEL--KLQL---AKKEEELQAALARAEEEAAQKNL 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 -- AQQHAQMEIPTMSHQLIGT 192
                                                        26/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176/3; 369/3; 449/3; 495/1; 528/1; 552/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
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                          glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTRHSQYVDAAPQA---YGSGQLVPENQRQPE----SAPDRP-YQIMNVGCNPQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                             hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 61.5; DB 2; 27.8%; Pred. No. 2.5e+02; tive 15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%; Score 61.5; 1
27.2%; Pred. No. 1e+0
tive 11; Mismatches
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33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endo-1,3-beta-glucanase; Osgl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                        from
probable DNA repair protein radC [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0007
                                                                                                        AB0007
                                                                                                                                  RESULT
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74

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R;Boegre, L; Jonak, C.; Mink, M.; Meskiene, I.; Traas, J.; Ha, D.T.C.; Swoboda, I.; Plar Plant Cell 8, 417-428, 1996
A;Title: Developmental and cell cycle regulation of Alfalfa nucMs1 a plant homolog of the A;Reference number: Z16796; MUID:96361876; PMID:8721748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: numr
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-635 <BOE>
A;Cross-references: UNIPROT:Q40363; UNIPARC:UPI00000AA67F; EMBL:X88845; NID:g1279562; PII
밁
                                                                                                                                                                                                                     A;Cross-references: UNIPROT:059744; UNIPARC:UPI000006B51D; A;Experimental source: strain 972h-; cosmid c530
                                                                                                                                                                                                                                                                                                                                                     R;Lyne, M.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, May
                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPBC530.08 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                  A;Reference number: Z21934
A;Accession: T40524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T40524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: nuM1 protein
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                                                                                                                                                                                                                                                            A;Residues: 1-815 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                               ;Map position:
;26-62/Domain:
                                                                                                                                                                                    Gene: SPDB:SPBC530.08;
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Best Local Similarity
Matches 12; Conserv
                                                                         Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                       Genetics:
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Best Local
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15; Conserv
                                                                         20;
                                                                                           Similarity
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 EADSPAMQALKVPDR--QTAFTLACKCVDSAIVCVQNLSHLSKGLKRTLD
                                  EIDGPAGQA--EPDRAHYNIVTFCCKCDSTLRLCVQS-THVD---IRTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPAKNGNVKKAOPETTS--EESDSDDISSDEEEVKKPAAKAVPSK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPTLHEYMLDLOPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDR
                                                                                                                                     GAL4 zinc binuclear cluster homology <GL4>
                                                                                                                                                                                                                                                                               DNA
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                                                                         Conservative
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                                                                                       11.8%;
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28.6%;
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                                                                         6;
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                                                                       Score 61; DB 2;
Pred. No. 1.1e+0;
6; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 2; Length 635; Pred. No. 86; B; Mismatches 20; Indels
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                         Barrell, B.G.;
1998
                                                                                         le+02;
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                                                                                                          Length 815;
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                                                                           Indels
                                                                                                                                                                                                                                            EMBL:AL023634; PIDN:CAA19174.1
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R; Parkhill, J.;

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hypothetical protein ZK632.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #te
C;Accession: S40936
R;Berks, M.
submitted to the EMBL Data Library, February 1993
A;Reference number: S40933
A;Reference number: S40933
A;Accession: S40936
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <BER>
A;Residues: 1-411 <BER>
A;Residues: 1-411 <BER>
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A;Residues: 1-411 <BER>
A;Residues: 1-411 <BER>
A;Residues: 1-411 <BER
                                                                                                                                                    A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: gee websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: C89134
                                                                                                                                                                                                                                                                                                           protein F25G6.6 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: C89134 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
C89134
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S40936
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A;Molecule type: DNA
A;Molecule type: CAUR>
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q8ZJP3; UNIPARC:UPI00001330CE; GB:AL590842; PIDN:CAC88916.1
C;Genetics:
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C;Superfamily: DNA repair protein radc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0007
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C;Superfamily: yeast mannose-6-phosphate isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             묽
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                                                              A; Molecule type: DNA
A; Residues: 1-551 <STO>
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C;Genetics:
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Cross-references: UNIPROT:016924; UNIPARC:UPI0000080118; Note: Similar to asparagine synthetase; F25G6.6
                                                                                                                                Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 CKC----DSTLRLCVQSTHVDIRTLEDLL 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Pred. No. 6
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Pred. No. 31;
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                             GB:chr_V; PIDN:AAC25799.1;
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N;Contains: SIL protein, short form
C;Species: Homo sapiens (man)
C;Date: 17-Unl-1992 #sequence_revision 17-Unl-1992 #text_change 09-Unl-2004
C;Accession: A41685
R;Aplan, P.D.; Lombardi, D.P.; Kirsch, I.R.
MO1, Cell. Biol. 11, 5462-5469, 1991
A;Title: Structural characterization of SIL, a gene frequently disrupted in A;Reference number: A41685; MUID:92017825; PMID:1922059
A;Accession: A41685
A; Molecule type: mRNA
A; Residues: 1-1287 - AAPL>
A; Cross-references: UNIPROT: Q15468; UNIPARC: UPI0000072CA6;
A; Note: exon/intron borders were determined by genomic DNA
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                   RESULT 78
A41685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; MOLECULO '4F-
A; Residues: 1-1269 < YAS>
A; Cross-references: UNIPROT: 043993;
A; Cross-references: UNIPROT: 043993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yasukawa, ..., EMBL Data submitted to the EMBL Data
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A;Gene: F25G6.6
A;Map position: 5
C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T14476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pslA protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
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;1-1287/Product: SIL protein #status predicted <MAT>
;1-165,213-1287/Product: SIL protein, short form #st
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24.4%; Pred. No. 2.10
tive 17; Mismatches
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Pred. No. 8
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   #status predicted
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                                                                           291/2; 341/3; 378/2;
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Query Match

11.7%;

Score 60.5;

BB

2

Length 1287;

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A; MOLTECUAL VIET.
A; Residues: 1-1826 <STO>
A; Cross references: UNIPROT: Q9Z985;
A; Cross references: Btrain J138
                                                                                                                                                                                                                                                                                                                                                                                                        R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: H86502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             excinuclease ABC subunit A [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (C;Dace: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: H86502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Anas sp.
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004 C;Accession: I50090
R;Kuroki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.
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C;Superfamily: Chlamydia trachomatis probable excinuclease ABC chain A; ATP-binding cas
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kuroki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.
J. Biol. Chem. 270, 15022-15028, 1995
A;Title: gp180, a host cell glycoprotein that binds duck hepatitis B virus particles, A;Reference number: A57010; MUID:95318059; PMID:7797483
                                                                                                                                                                                                                                                                                     A; Experimental source: strain C; Genetics:
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A; Residues: 1-1389 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   र्
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q90240; UNIPARC:UPI00000FC41C; EMBL:U25126; NID:g1008477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I50090
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                                                                                                                                                              Query Match
Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                            877 DYVLELGPEGGDLGGYLLASCTPKDLIQLNTPTAKALAPYIEGSLDIPVVKSEPPSSPKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                    54 IVTFCCKCDSTLRICVQST--HVDIRTLEDLLMGTLG
                                                                                                                   10 EYMLDLQPETTDLYXY------XQLNDSSEE-----EDEIDGPAGQAEPDRAHYN 53
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                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGGGEGGEP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGDEPLARPLLIRLAQELVRGWAGGDERLGRLLNTTDLYLLPSLNPDGFERAREGDCGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGLLÓSSÓNSEDEEEPPDNÁDSKSEYLLNONLRSIPEQLGGÓKEPSKNDHEIIN-CSNCE 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YXYXQLNDSSEEEDEIDGPA----
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                                                                                                                                                              Conservative
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-CDILIKDAYONNLKHIDLALPRNSLIAIAG
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                                                                                                                                                                17;
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1; Mismatches
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                                                                                                                                                                               Score 60.5; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.1e+02;
1; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                            UNIPARC: UPI000016569B; GB: BA000008; NID: 98978469;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3e+02;
ches 23;
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                                                                                                                                                              32;
966
                                                                                                                                                                                                    Length 1826;
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                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.; Ouchi, K.; Shiba,
                                                                                                                                                              25;
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                                                                               936
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A;Cross-references: UNIPROT:049909; UNIPARC:UPI00000AC71C; EMBL:Y12806 A;Experimental source: strain petit havana C;Superfamily: Ripening-related protein-like, contains similarity to p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invertase inhibitor homolog - common tobacco
c;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T03396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: uvrA; CP0678
C;Superfamily: Chlamydia trachomatis probable excinuclease ABC chain A;
F;609-885/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1826 <REA>
A;Cross-references: UNIPARC:UPI0000137E7B; GB:AE002226; GB:AE002161; NID:g7189592; PIDN:I
A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1826 <ARN>
A;Cross-references: UNIPROT:Q92985; UNIPARC:UPI0000137E7B; GB:AE001595; GB:AE001363; NID A;Cross-references: UNIPROT:Q92985; UNIPARC:UPI0000137E7B; GB:AE001595; GB:AE001363; NID A;Cross-references train CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, F.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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   片
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z14924
A; Accession: T03396
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Greiner, S.; Krausgrill, S.; Rausch, T. submitted to the EMBL Data Library, April
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Best Local Similarity
                                                                                                                                                                        Query Match
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                                                                                                                                             Local
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24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 EYMLDLQPETTDLYXY------XQLNDSSEE-----EDEIDGPAGQAEPDRAHYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                      1-172 <GRE>
                                                                                                                                          Similarity
                                                      NIVTECCKCDSTLRLCVQSTHVDIRTLE----DLLMGTLGIV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYVLELGPEGGDLGGYLLASCTPKDLIQLNTPTAKALAPYIEGSLDIPVVKSEPPSSPKS
   NIINTTCRATTNYPLCLTTLHSDPRTSEAEGADLT--TLGLV 63
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23.7%;
                                                                                                                                          38.1%;
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; Pred. No. 3e+02;
17; Mismatches 32;
                                                                                                                                          Score 60;
Pred. No.
                                                                                                            Pred. No. 27;
6; Mismatches
                                                                                                                                                DB 2; Length 172, 27;
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RESULT

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C;Accession: H86352
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authores Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authores Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Ascession: H86352
A;Status: preliminary
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary;
A;Status: preliminary;
A;Status: preliminary;
A;Residues: 1-370 <AQF>
A;Residues: 1-370 <AQF>
A;Cross-references: UNIPROT:066761; UNIPARC:UPI0000056374; GB:AE000690; GB:AE000657;
A;Experimental source: strain VF5
C;Genetics:
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A;Reference number: A70300; MUID:98196666; PMID:9537320
$46281
P element - fruit fly
C;Species: Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein F2E2.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein aq_454 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: E70341
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C; Superfamily: Ar
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A; Residues: 1-465 <STO>
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C;Superfamily: conserved hypothetical protein yodO
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                                                                                          RESULT 85
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: F2E2.2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                             233 DTPSLVYLDYSGHVARRYTAEMGSLEEARLNLLPWEQLIDSDEEDDDFDGYGPRWEKRSK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
27; Conserv
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Similarity 33.3%;
                                                                                                                                                                                                                                 HYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                   DTPTL-----HEY---MLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DALKEEGDIPG-LTHRYPDRVLLNVTTFCAVYCRHCMRKRIFSQGERARTKEEI 146
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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         (Drosophila
bifasciata
                                                                                                                                                                                 DATGLIAMIS---NVKTLH-LSSDSLEVIHSLCKVMP
                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 60; DB 2; Length 465; 25.0%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                               17;
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                                    ananassae)
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: $46281  
R;Hagemann, S.; Miller, W.J.; Pinsker, W. Mol. Gen. Genet. 244, 168-175, 1994  
Mol. Gen. Genet. 244, 168-175, 1994  
A;Title: Two distinct P element subfamilies in the genome of Drosophila bif; A;Reference number: $46281; MUID:94329069; PMID:8052236  
A;Accession: $46281
                                                                                                                     R;Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, M.J. Biochem. Biophys. Res. Commun. 233, 537-544, 1997
A;Title: Identification and cDNA cloning of a novel mammalian C2 doma A;Reference number: JC5500; MUID:97289668; PMID:9144573
                                                                                                                                                                                                                        phosphoinositide 3-kinase (EC 2.7.1.-) - human C;Species: Homo sapiens (man) C;Dspecies: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: JC5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: supposed to play a role in anchoring the terminal A;Note: specifically expressed in skeletal and cardiac muscle C;Keywords: skeletal muscle; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Luo, G.; Zhang, J.Q.; Nguyen, T.P.; Herrera, A.H.; Paterson, B.; Horowits, R. Cell Motil. Cytoskeleton 38, 75-90, 1997
A;Title: Complete cDNA sequence and tissue localization of N-RAP, a novel nebulin-related A;Reference number: Z21630; MUID:97439586; PMID:9295142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nebulin-related protein, skeletal muscle - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37192
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A;Residues: 1-1634 <BRO>
A;Cross-references: UNIPROT:000750;
A;Experimental source: breast cell
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A; Residues: 1-1175 < LUO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A; Residues: 1-562 < HAG>
                                                                         A; Molecule type: mRNA
                                                                                                   A; Accession: JC5500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 DGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CVQSTHVDIR 77
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 2; L. Pred. No. 2.1e+02; B; Mismatches 37;
                          UNIPARC: UPI000013185A;
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                            GB:Y11312;
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                          NID: 92808446;
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coat protein - pelargonium leaf curl virus
C;Species: pelargonium leaf curl virus
C;Accession: A48355
R;Li, Y. Bachmann, S.; Maiss, E.; Commandeur, U.; Breyel, E.; Timpe, U.; Koenig, R.
Arch. Virol. 129, 349-356, 1993
A;Title: Nuclectide sequence of the coat protein gene of pelargonium leaf curl virus and A;Reference number: A48355; MUID:93228459; PMID:8470957
A;Accession: A48355
A;Molecule type: genomic RNA
A;Residues: 1-389 <LLI>A;Cross-references: UNIPROT:Q86586; UNIPARC:UPI00000F7BB9; GB:858174; NID:g299096; PIDN:
A;Kote: sequence extracted from NCBI backbone (NCBIN:129117, NCBIP:129118)
C;Superfamily: carnation mottle virus coat protein
C;Keywords: coat protein; glycoprotein
F;8,9,117,118,139.357/Pi-A-J
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C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase
C;Keywords: phosphotransferase
F;156-162,169-174/Domain: SH3 #status predicted <SH3>
F;1037-1320/Domain: catalytic #status predicted <CAT>
F;10498-1612/Domain: protein kinase C C2 region homology <KC2A>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 109/3; 168/3; 222/1; 235/1
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YPL096w
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A;Residues: 1-333 <LYN>
A;Residues: 1-333 <LYN>
A;Cross-references: UNIPROT:074739; UNIPARC:UPI000006C436; EMBL:AL031852; PIDN:CAA21253
A;Experimental source: strain 972h-; cosmid c1709
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein SPBC1709.14 - fission yeast (Schizosaccharom C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 LHEINIEFRSRLTDSERKALEEEDKREKDELDGYMRPVSQATP 309
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ilarity 32.6%;
Conservative
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25.8%;
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Pred. No. 3.1e+02
L7; Mismatches 3:
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Pred. No. 63
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; E ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.R.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: C96640
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Best Local S
Matches 26
                                                                                                                                                                                                                                                                               Status: preliminary
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26; Conserv
                                                                                                  Similarity
TMALHNYIRDSQQEDSDFRHWEIVESYEQHGDENDGHVPYVPTG----DRVMENI 388
                                     TPTLHEYMLDLOPETTDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAHYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEATLNIPCDRIKRYCDDSATVDHKLID---LGQLGI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQYTFNNVVLHYVPLCATTEVGRVAMYFDKDSEDVE---PADRVE--LANYGVLKETAPW 208
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                                                                             Conservative
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                                                                                                11.5%;
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26.8%; Pred. No. 74;
tive 13; Mismatches
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Pred. No. 77;
5; Mismatches
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Dewar, K.;
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tungsten formylmethanofuran dehydrogenase, subunit F (fwdF) homolog - C_i Species: Archaeoglobus fulgidus C;Accession: C69455 Archaeoglobus Dodson, fulgi

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69455

A;Residues: A; Molecule type: DNA A;Status: preliminary; nucleic acid sequence not shown; translation not 1-438 <KLE>

shown

A;Cross-references: UNIPROT:028629; UNIPARC:UPI000056C46; GB:AE000989; GB:AE000782; C;Superfamily: formylmethanofuran dehydrogenase, subunit F; ferredoxin 2[4Fe-4S] home F;28-94/Domain: ferredoxin 2[4Fe-4S] homelogy <FFR3> Query Match Similarity 11.5**%**; 21.3**%**; Score Pred. No. 84; 80 2 Length 438

70

OSTHVDIRTLEDLIMGTLGIVXPICSOK

97

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C;Accession: A85438
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr. Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A85438
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-596 <STO>
A;Cross-references: UNIPROT:023178; UNIPARC:UPI00000986AC; GB:NC_001268; NID:97270657; C;Genetics:
                                                                                                                                A;Gene: AT9937000
A;Map position: 4
C;Superfamily: Putative ternary complex factor MIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AT4g37080 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004 C;Accession: A85438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:084760; UNIPARC:UPI00000D339E; GB:AE001348; GB:AE001273; A;Experimental source: serotype D, strain UW-3/Cx C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 C;Accession: B71474 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Pan, J.; Marathe, R.; Aravind,
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EAAADKHSESTKLQLDDRLADQDKAQESVSGSSSE--
                                          EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCV 69
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24.3%; Pred. No. 16
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                                                                                                       Score 59.5; DB 2;
Pred. No. 1.2e+02;
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1; Mismatches
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C; Paccession: E96793
C; Accession: E96793
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Asture 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A; Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37-C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokin C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 152, 181-186, 1995
A;Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophosp
A;Reference number: Z16949; MUID:95137384; PMID:7835697
                                          8
                                                                                                                                                                                                   A;Map position: 1
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
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                                                                                                                                                                                                                                                                  A;Gene: F14G6.15
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A; Residues: 1-617 <STO>
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                                                                                                                                                                                                                                                                                                 ;Genetics:
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;Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
                                                                                                      Matches
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Best Local !
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                                                                                                                                                         Query Match
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505 PVIHPASVDLKGKAYDL----LRQNAQKFLMEDMYRNPGPVQYDGPGADAK----
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                         PTLHEYMLDLQPETTDLYXYXQLNDSSEE---ED-----
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                                                                                                   11.5%; Score 59.5; DB 2; 24.0%; Pred. No. 1.2e+02; tive 15; Mismatches 29;
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Pred. No. 1.2e+02;
5; Mismatches 33;
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                                                   --- SIDGPAGQAEPDRAHYNI 54
                                                                                                                                                         Length 617;
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A;Molecule type: DNA
A;Residues: 1-1708 <MTH>
A;Residues: 1-1708 <MTH>
A;Cross-references: UNIPROT:026769; UNIPARC:UPI0000066625; GB:AE000847; GB:AE000666;
A;Experimental source: strain Delta H
C;Genetics:
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F69189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: F69189
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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R;Rounsley, S.D; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, April 1998
A;Description: Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence.
A;Reference number: Z14153
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A;Molecule type: DNA
A;Residues: 1-822 <STO>
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                                                                                                                                                                                                    Gene: MTH673;Superfamily: Methanobacterium thermoautotrophicum
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    Similarity 23.9
28; Conservative
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11.5%; Score 59.5; DB 2; 23.9%; Pred. No. 3.7e+02; ive 12; Mismatches 46;
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hypothetical 527K polyprotein
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wyosin heavy chain, nonmuscle - chicken N;Contains: myosin ATPase (EC 3.6.4.1) C;Species: Gallus gallus (Chicken) C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: A33977; S06116; Ā43422 R;Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S. Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989 A;Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular: A;Reference number: A33977; MUID:90046668; PMID:2813355 A;Accession: A33977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000008A46C
A;Experimental source: brush boxder
A;Experimental source: brush boxder
A;Note: sequence extracted from NCBI backbone (NCBIP:111947)
A;Note: sequence extracted from NCBI backbone (NCBIP:111947)
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI0000173E31; GB:X17589
A;Note: this translation is not annotated in GenBank entry GGMHCFMHA, release R;Hodge, T.P.; Cross, R.; Kendrick-Jones, J.
J. Cell Biol. 118, 1085-1095, 1992
A;Title: Role of the COOH-terminal nonhelical tailpiece in the assembly of a v A;Reference number: A43422; MUID:92381096; PMID:1512291
A;Accession: A43422
A;Status: nucleic acid sequence not shown; not compared with conceptual transl A;Residues: 1900-1959 <HOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1959 <5HO>
A;Cross-references: UNIPARC:UPI000012FB7F;
R;Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs as
                                                                                                                                                                                                                                    F;1278-1959/Region: light meromyosin F;1937-1959/Domain: carboxyl-terminal <CBT> F;125/Modified site: N6, N6-trimethyllysine () F;180/Binding site: ATP (Lys) #status predicted F;694,704/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         F;552-565/Region: actin binding #status predicted F;626-640/Region: actin binding #status predicted cOI.
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A; Residues: 716-1008 < KAT>
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LEGDSSDLHDQIAELQAQIAEL--KIQL--
                                                     MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNI 54
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14; Mismatches
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Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Recession: AF1164
A;Recession: AF1164
A;Retatus: preliminary
A;Molecule type: DNA
A;Residues: 1-214 cGIA>
A;Residues: 1-214 cGIA>
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A;Molecule type: DNA
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A;Molecule type: DNIPAC: UNIPARC: UPI00001101CF; EMBL: D32136; NID: g511666; PII
A;Cross-references: UNIPROT: Q40712; UNIPARC: UPI00001101CF; EMBL: D32136; NID: g511666; PII
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A;Note: only a part of the coding sequence is given
R;Fukuhara, T: Moriyama, H: Pak, J.Y: Hyakutake, H: Nitta, T.
Plant Mol. Biol. 21, 1121-1130, 1993
A;Title: Enigmatic double-stranded RNA in Japonica rice.
A;Reference number: S33529; MUID: 93257627; PMID: 8490131
A;Accession: S33529
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 3854-4370 <FUK>
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1164
C;Accession: AF1164
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Jones, L.M.; Karst, U.
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C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57908; S33529
R;Moriyama, H.; Nitta, T.; Fukuhara, T.
Mol. Gen. Genet. 248, 364-369, 1995
A;Title: Double-stranded RNA in rice: a novel RNA replicon in plants.
A;Reference number: S57908; MUID:96004703; PMID:7565598
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C; Keywords: polyprotein
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: rice hypothetical 527K polyprotein
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;Experimental source: strain EGD-e
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71-FEB-2006, 0
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STRAIN-Isolate African 1, and Isolate European German 131;
Terai M., Fu L., Ma Z., Burk R.D.;
"Cloning and sequencing of non-European human papillomavirus
"Cloning and sequencing of cervicovaginal cells by an over
                            TEMB1;
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Phelps W.C., Yee C.L., Munger K., Howley P.M.;
"The human papillomavirus type 16 E7 gene encountries that to those of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].

Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang Submitted (NOV-1996) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBa
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"Expression of the human papillomavirus type 
a line derived from a vulvar intraepithelial 
J. Gen. Virol. 71:809-817(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 53:539-547(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Tornsello M.L., Buonaguro F.M., M
Beth-Giraldo E., Giraldo G.,
Submitted (JUN-1997) to the EMBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85246220; PubMed=2990099;
Seedorf K., Krammer G., Durst M.,
"Human papillomavirus type 16 DNA
Virology 145:181-185(1985).
                                                                                                                                                                                                                                                                                                                             Copyrighted
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MEDLINE=90218027; PubMed=2157796;
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MEDLINE=85246220; PubMed=2990099;
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MBL; K02718; AAA46940.1; -; Genomic_DNA.
MBL; U076411; AAB18962.1; -; Genomic_DNA.
MBL; U76411; AAB18963.1; -; Genomic_DNA.
MBL; U76412; AAB18963.1; -; Genomic_DNA.
MBL; U76413; AAB18964.1; -; Genomic_DNA.
MBL; AF003020; AAB70737.1; -; Genomic_DNA.
MBL; AF003023; AAB70740.1; -; Genomic_DNA.
MBL; AF003024; AAB70741.1; -; Genomic_DNA.
MBL; AF003025; AAB70741.1; -; Genomic_DNA.
MBL; AF003025; AAB70743.1; -; Genomic_DNA.
MBL; AF003025; AAB70743.1; -; Genomic_DNA.
MBL; AF536189; AAG70743.1; -; Genomic_DNA.
MBL; AF536189; AAG70743.1; -; Genomic_DNA.
MBL; AF536189; AAG70713.1; -; Genomic_DNA.
MBL; AF536189; AAG70721.1; -; Genomic_DNA.
MBL; AF536189; AAG70721.1; -; Genomic_DNA.
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es, no RNA stage;
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Attribution-NoDerivs License
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Cype 16 genome in S
lial neoplasia.";
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databases.
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RESULT 3
Q778G4 HPV16
ID Q778G4 HPV16
AC Q778G4;
DT 10-MAX-2005,
DT 10-MAX-2005,
DT 07-FEB-2006,
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Q547B8 H
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF512012; AAM74160.1; -; Genomic_DNA. GO; GO:0005622; C:intracellular; IEA. GO; GO:0003700; F:transcription factor activity; GO; GO:0006355; P:regulation of transcription, DN NON_TER 98 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type
Viruses; dsDNA viruses no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-2005, integrated into 1
24-MAY-2005, sequence version
07-FEB-2006, entry version 3.
E7 protein (Fragment).
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Zhang, J, Gao, Y, Yan
"Cloning and sequence
in China.";
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DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN 1 98 Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQXP
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analysis
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/FTIG=PRO_0000133414.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.

CPXX-C motif-2.
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Pred. No. 4.
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integrated into l sequence version entry version 3.

PRELIMINARY;

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RESULT 4
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor acti
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GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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Pred. No. 4.
                                                                                                                                                              ion factor activity; IBA.
of transcription, DNA-dependent;
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                                                                                                                                                                10-MAY-2005, integrated into 1 10-MAY-2005, sequence version 3. 07-FEB-2006, entry version 3. E7 protein (Fragment).
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MEDLINE=20112892; Pubmed=10644829;

WEDLINE=20112892; Pubmed=10644829;

van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E7 protein (Fragment).
Human papillomavirus type 16
Viruses, dsDNA viruses, no R
                                                              Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
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Q778G9;
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NCBI_TaxID=333760;
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor acti
GO:0006355; P:regulation of transcripti
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GO:0005622; C:intracciption factor activity; IEA.
GO:000370; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Q778H7 HPV16 PRELIMINARY; P
Q778H7;
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10-MAY-2005, sequence version 1
07-FEB-2006, entry version 3.
E7 protein (Fragment).
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H2 HPV16
Q778H2 HPV16
                                                                MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Verheijen R.H., Helmerhorst T.J., Meijer "Analysis of human papillomavirus type 16 p53 codon 72 polymorphism genotypes in ce J. Gen. Virol. 81:317-325(2000).
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=20112892; PubMed=10644829;

MEDLINE=20112892; PubMed=10644829;

van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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GO:0005622; C:intracellular; IEA.
GO:0003700; Fitranscription factor activity;
GO:0006355; P:regulation of transcription, Dx
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GO:0005622; C:intracellular; IEA.
GO:000370; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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GG:0005622; G:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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PF00527; E7; 1;
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PF00527; E7; 1.
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Pred. No. 4.5e-52;
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I(1) HPV16
Q778I1 HPV16
Q778I1;
10-MAY-2005, integrated into UniProtKB/TrEMBL.
10-MAY-2005, sequence version 1.
07-FEB-2006, entry version 3.
Pfam; PI
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
Pfam; PF00527; E7; 1.
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MEDLINE=20112892; PubMed=10644829;

WED Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation

"Analysis of human papillomavirus type 16 E6 variants in relation

p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                     MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F. Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; Panalysis of human papillomavirus type 16 E6 variants in relation p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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                                                                                 EMBL, AJ388058; CAB45109.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E7 protein (Fragment)
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RESULT 14
Q77815 HPV16
ID Q77815; HPV16
AC Q77815;
DT 10-MAY-2005, i
DT 10-MAY-2005, o
DT 07-FEB-2006, e
DE E7 protein (Fr
OS Human papilloma
OC Viruses; dsDNA
OC Alphapapilloma
OX NCBI_TaxID-333
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Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.,
"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.",
J. Gen. Virol. 81:317-325(2000).
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GO:0003700; F:transcription factor activity; IEA.
GO:006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                             L; AJ242681; CAB45382.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:000370; F:transcription factor activity; IEA.
GO:0003355; P:regulation of transcription, DNA-dependent;
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  Score
Pred.
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Pred. No. 4.
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                                                                                 9BD612534CD2C9EB
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factor activity; ILA.
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512;
No. 4
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4.5e-52;
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777GV7 HPV16
PRELIMINARY; PRT; 98 AA.
077GV7;
10-MAY-2005, integrated into UniProtKB/TrEMBL
10-MAY-2005, sequence version 1.
07-FEB-2006, entry version 7.
                                                                                                                                                                                                                          QEH-1220, QEH-400, PWH-Q27, QEH-318, and PWH-Q39; QEH-1220, QEH-400, PWH-Q27, QEH-318, DOI=10.1086/342048; Chen P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W., Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infectior cervical neoplasia in southern China.";
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NUCLEOTIDE SEQUENCE.
MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
DeFilippis V.R., Ayala F.J., Villarreal L.P.;
"Evidence of diversifying selection in human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868; Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.; "Establishment of the human papillomavirus type 16 (HPV-16) life cycle in an immortalized human foreskin keratinocyte cell line.";
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STRAIN=QEH-2076, QEH-186, PWH-Q42,
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Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Z., Terai M., Fu L., Herrero R., DeSalle R., Burk "Diversifying selection in human papillomavirus type 1 on complete genome analyses.";
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Submitted
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Distributed
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(JUL-2001)
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       ; AAO85409.1; -; (AAV91653.1; -; (AAV91661.1; -; (AAV91669.1; 
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                                                                                                                                  see http://www.uniprot.org/te
Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus. NCBI_TaxID=333760;
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GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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Ol-JUL-1997, sequence version
Ol-FEB-2006, entry version 24.
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Submitted (AUG-2002)
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MEDLLNE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;

Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
Lee H.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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AF4863312;
AF4863323;
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ilarity 95.9%;
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H3 HPV16
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Q778H3;
05-JUL-2004, i
05-JUL-2004, i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003700; F:transcription of transcription, DI
InterPro; IPRO00148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CF
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MEDLINE=20112892; PubMed=10644829;
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integrated into I sequence version

UniProtKB/TrEMBL

PRELIMINARY;

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RESULT 21

QBQRD2_HPV16

ID QBQRD2;

DT Q1-JUN-2002, integrated into UniProtKB/TrEMBL.

DT Q1-JUN-2002, sequence version 1.

DT Q1-JUN-2002, sequence version 1.

DT Q1-JUN-2002, sequence version 10.

E7 protein.

DE B1-2006, entry version 10.

E7 protein.

ON Human papillomavirus type 16.

OC Viruses; dSDNA viruses, no RNA stage; Papillomavi OC Alphapapillomavirus.

OX NCBL TaxID=333760;

RN [1] - TaxID=333760;

RN (1] - TaxID=333760;

RN MUCLEOTIDE SEQUENCE.

RA MEDLINE=22102962; PubMed=12195358; DOI=10.1086/34

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lc

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lc

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lc

RA Chan papillomavirus type 16 intratypic variant

for cervical neoplasia in southern China.";

RI J. Infect. Dis. 186:656-700(2002).

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Pfam; PFOC
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MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., C
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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PF00527; E7; 1.
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Pred. No. 1.7e-51;
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Query Match

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AC Q2Z

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                                                                                  Human papillomavirus typ
Viruses; dsDNA viruses,
Alphapapillomavirus
NCBI_TaxID=333760;
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01-JUN-2002,
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NCBI_TaxID=333760;
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Viruses; dsDNA viruses, no
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   NUCLEOTIDE SEQUENCE.
Meshkat Z., Hassan Z.M.,
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GO; GO:0006355; P:regulation of transcription, DNA-dependent;
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Pfam; PF00527; E7; 1.
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1; Mismatches
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Pred. No. 1.7e-51;
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RESULT 24
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1D 012338;
DT 01-JUL-1997, i
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DE E7 protein.
OS Human papillom
OC Viruses; dsDN/2
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OC NCBI_TAXID=333
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EMBL; AF477385; AAM03025.1; -; Genomic_DNA.
EMBL; AF477385; AAM03025.1; -; Genomic_DNA.
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
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Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of hum
type 16 in penile carcinomas from Ugandan patients.
J. Gen. Virol. 78:2199-2208(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
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MEDLINE=97437474; PubMed=9292007;
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01-JUL-1997, sequence version
07-FEB-2006, entry version 20
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                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 16.
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in Iran."
                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                    InterPro; IPR000148; Papvi_E7.
61
                            61
                                                                                                                                                                                         PF00527; E7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQ323401; ABC54573.1; -; Genomic DNA.
NCE 98 AA; 10992 MW; 9BD6125357D379EB CRC64;
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                                                                                                                             94;
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                                                                                                                          Similarity 95.9
94; Conservative
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                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CDSTLRLCVQSTHVDICTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                          E7;
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                                                                                                                                                                                           10969 MW;
                                                                                                                                        97.5%;
95.9%;
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95.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no RNA stage; Papillomaviridae;
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                                                                                                                          Score 504; DB 2;
Pred. No. 3.9e-51;
0; Mismatches 4
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Pred. No. 1.7e-51;
0; Mismatches 4
                                                                                                                                                                                            9BD612534CCEA59B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meglio A., Buonaguro
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                                                                                                                                                                                            CRC64;
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98
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RESULT 26
QBQRD4 HPV16
QBQRD4;
AC QBQRD4;
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2012, s
DC Viruses; dsDNJ
OC Viruses; dsDNJ
OC Viruses; dsDNJ
OC VIRUSes; dsDNJ
OC VIRUSes; dsDNJ
OC VIRUSes; dsDNJ
OC VIRUSes; dsDNJ
OC VIRUSes; dsDNJ
OC NGBI TAXID=33;
RN [1]
CR NGLING=22182;
RA Chan P.K.S., I
RA Cheung J.L.K.,
RT for cervical 1
RL J. Infect. Dist
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CC MICHIGAN
DR GO; GO:000562;
DR GO; GO:000562;
DR GO; GO:0006370
DR GO; GO:0006370
DR Pfam; PF00527
SQ SEQUENCE 98
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Q8VLJO_HPV16
ID Q8VLJO;
AC Q8VLJO;
DT 01-MAR-2002, 6
DT 07-FEB-2006, 6
DE E7 protein.
OS Human papillom
OC Viruses; dSDNP
OC Alphapapilloma
OX NCBI_TAXID=333
RN [1]
CR NUCLEOTIDE SEC
RA Jinhu X. Xinx
RL Submitted (DEC
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CC DR GO:0006355
DR GO:0006355
DR FEMBL; AF461264
DR GO; GO:0006355
DR InterPro; IPRO
DR Pfam; PF00527;
SQ SEQUENCE 98
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Best Local :
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01-JUN-2002,
07-FEB-2006,
                                        EMBL; AF486329; AAL96634.1; -; Genomic_DNA.
GO; GC:0005622; C::intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:regulation of transcription, DNA-dependent;
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.

MEDILINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cl
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection of the cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
      Pfam; PF00527; E7; SEQUENCE 98 AA;
                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=333760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF461264; AAL66736.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003755; P:regulation of transcription, DNA-de
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Viruses; dsDNA viruses, no Rh
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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10997 MW;
      11025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 version
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94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA stage; Papillomaviridae;
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Pred. No. 1.
         86E24B234CC3281B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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RESULT 27
QBB5P6 HPV16
ID QBB5P6 H
AC QBB5P6;
DT 01-MAR-2
DT 01-MAR-2
DT 07-PEB-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-MAR-2
DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT 01-DT
RESULT 28
Q9QDH6 H
AC Q9QDH6;
DT 01-MAY-2
DT 01-MAY-2
DT 07-FEB-2
DT 07-FEB-2
DE E7 prote
OS Human pa
OC Viruses;
OC Alphapap
OC NCBI_Tax
RN [1]
RA Lee H.F.
RL Submitte
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                                                                                                                                                                                                                                                   QJQDH6 HPV16 PRELIMINARY;
QJQDH6;
Q1-MAY-2000, integrated into U
01-MAY-2000, sequence version
07-FEB-2006, entry version 14.
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                                                                                                                                                     Human papillomavirus type 16. Viruses; dsDNA viruses, no Rh Alphapapillomavirus.
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                          NUCLEOTIDE SEQUENCE.
Lee H.P., Song Y.S.,
Submitted (SEP-1999)
                                                                                                                     NCBI_TaxID=333760;
                                                                                                                                                                                                                              E7 protein (Fragment).
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G0:0005622; C:intraccellular; IEA.
G0:0003700; F:transcription factor activity; IEA.
G0:0006355; F:regulation of transcription, DNA-dependent;
erPro; IPR000148; Papvi_E7.
mr; PP00527; E7; 1.
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ilarity 94.9%;
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                          Kim J.W., Roh J.W., Park N.H., Kang S.B.; to the EMBL/GenBank/DDBJ databases.
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1; Mismatchès 4
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Pred. No. 4.9e-49;
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RESULT 30 Q9QDH4 HPV16 ID Q9QDH4 H AC Q9QDH4; DT 01-MAY-2 DT 01-MAY-2

PRELIMINARY;

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Q9QDH4 HPV16 Q9QDH4; 01-MAY-2000, 01-MAY-2000,

sequence version

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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF187869; AAF13399.1; -; Genomic_DNA. GO; GO:0005622; C:intracellular; IEA. GO; GO:0003700; F:transcription factor activity; IEA. GO; GO:0006355; P:regulation of transcription, DNA-dependent;
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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0; Mismatches
                                                                                                                                                                                                    Score 477; DB 2; I
Pred. No. 5.6e-48;
1; Mismatches 3;
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No. 4.2e-48;
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Best Local Similarity
Matches 89; Conserv
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SEQUENCE
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QQQDH8;
Q1-MAY-2000, integrated into U
01-MAY-2000, sequence version
Q7-FEB-2006, entry version 14.
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.

Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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Lee H.P., Song Y.S.,
Submitted (SEP-1999)
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NCBI_TaxID=333760;
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E7 protein (
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31
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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PF00527; E7; 1.
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68
                                                                                                                                                                     Similarity
                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                               IPR000148; Papvi_E7.
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to the EMBL/GenBank/DDBJ databases.
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                                                                                                                       Score 477; DB 2; I
Pred. No. 5.6e-48;
1; Mismatches 3;
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Pred. No. 5.6e-48;
                                                                                                                                                                                                                                                                    83281BB2AE2C8A1F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULT 33
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Best Local
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07-FEB-2006, entry version 11.
E7 protein (Fragment).
Human papillomavirus.
Viruses, dsDNA viruses, no RNA sunclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                  Protein E7.
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VE7_HPV35
P27230;
                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE STRAIN=Isolate 35H;
                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
Alphapapillomavirus.
ACBI_TaxID=10587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF469198; AAO15694 1; -; Genomic DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activit;
GO; GO:0003750; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003,
Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.; "The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35.";
                                                                                                                                                                                       Delius H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Submitted (JAN-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10566;
                                                                   NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE=92124753; PubMed=1310198;
                                                                                                                                                                                                             MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                         "Primer-directed sequencing Curr. Top. Microbiol. Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00527; E7; 1.
ER 77 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                       Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AA; 8782 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             integrated into UniProtKB/Swiss-Prot. sequence version 1. entry version 32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                        [GENOMIC DNA]
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                                                                                                                                         encing of human papillomavirus Immunol. 186:13-31(1994).
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                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                    RNA stage;
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Pred. No. 1e-39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C5DE3A7E546AC31B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor activity; IEA.

Concernation, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                      Papillomaviridae;
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RESULT 34
Q76WP2 9PAPI
ID 6WP2;
AC Q76WP2;
DT 05-UUL-2004, s
DT 05-UUL-2004, s
DT 07-FBB-2006, c
DE E7 protein.
OS Human papillom
OC Viruses; dsbNn
OC unclassified p
OX NCBI TaxID=105
RN [1]
RN [1]
CC Copyrighted by
CC Copyrighted un
CC Distributed un
CC Distributed un
CC Distributed un
CC EMBL; D10597;
DR GO; GO:0005622
DR GO; GO:0005755
DR InterPro; IPRO DR Pfam; pF00527;
SQ SEQUENCE 99
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Best Local S
Matches 72
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Best Local (
                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; unclassified Papillomaviridae. NCBI_TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1. 07-FBB-2006, entry version 10.
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DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN 1 99 /FTTd=PRO 0000133433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMMBL; M74117; AAA46967.1; -; Genomic_DNA.
EMMBL; X74477; CAA52562.1; -; Genomic_DNA.
PIR; F40824; W7WLJS.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                               InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 99 AA; 10954 MW;
                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus.

    IL; D10597; BAA01448.1; -; Genomic_DNA.
    GO:0005622; C:intracellular; IEA.
    GO:0003700; Fitranscription factor activity; IEA.
    GO:0003700; Fitranscription for transcription, DNA-dependent;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
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                                                                                                                     . Similarity 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
               KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                        MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSS-EBEDBIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIGETITIODYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC
KCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQR
                                                          MHGEITTLODYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                     Conservative
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92
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95
10954 MW;
                                                                                                                                                                      1.
10954 MW; 8EAA8F248051E226 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.8%;
                                                                                                                                   73.8%;
73.5%;
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/FTId=PRO_0000133433.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                Score 381.5; DB 2;
Pred. No. 1.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1e
1; Mismatches
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Pred. No. 1.1e-36;
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 98
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RESULT 35
VE7_HPV31
ID VE7_HPV31
AC P17387;
DT 01-AUG-199)
DT 07-FB-200
DE Protein E7
GN Name=E7;
OS Human papi.
OC Viruses; d.
OC Alphappill
OC Alphappill
OX NCBI TAXID.
RN NICLECTIDE
RN NUCLECTIDE
RN WICLECTIDE
RN WICLECTIDE
RN WICLECTIDE
RY MEDLINE-89;
RA Goldsborow
RT neoplasia-
Virology 1:
CC -!- SIMILA
CC -!- SIMILA
CC -!- SIMILA
CC --- CCOpyrighte-
CC Copyrighte-
CC FMBL; J043
DR InterPro;
DR FIR; B3244
DR InterPro;
DR Pfam; PF00
DNA-bindin
KW Transcript
FT CHAIN
FT CHAIN
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FT MOTIF
FT MOTIF
SQ SEQUENCE
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01-AUG-1990,
07-FEB-2006,
                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL.
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
E7 transforming protein variant.
Human papillomavirus type 31.
Viruses, dsDNA viruses, no RNA stage: Panillom
                                                                                                                                                                                                              Q6T377_HPV31
Q6T377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viruses; dsDNA viruses,
Alphapapillomavirus
NCBI_TaxID=10585;
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                                        NUCLEOTIDE SEQUENCE.
Fiedler M., Fitzky B., D
Submitted (OCT-2003) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN 1 98 Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04353; AAA46951.1; -; Genomic_DNA.
PIR; B32444; WYWL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tonstributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 171:306-311(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type 31.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                 _HPV31
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                          69;
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                                                                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                       CKSTLRLCVQSTQVDIRILQELLMGSFGIVCPNCSTR
                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                               IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
91
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry version 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
94
10918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%;
                                          Durst M., Zwerschke W., Jansen-Du
o the EMBL/GenBank/DDBJ databases.
                                                                                                                               no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    has both transforming
                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein E7.
/FTId=PRO_0000133429
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 372; DB 1;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      793B7F5BC7324E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                   86
   see http://www.uniprot.org/terms
Attribution-NoDerivs License
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                                                           Jansen-Durr P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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RESULT 38
O90724 HPV67
ID 090724;
AC 090724;
DT 01-NOV-1998, 4
DT 07-FEB-2006, 6
DE ORF E7.
OS Human papillon
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IDBS63
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Best Local S
Matches 62
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Best Local Similarity
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63 9PAPI
QBB563 9PAPI
QBB563;
QBB563;
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N TER
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07-FEB-2006, entry vers
E7 protein (Fragment).
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:00003700; P:regulation of transcription, DNA-dependent;
InterPro; IPRO00148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10917 MW; 9D31DFF1CF9064B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ponglikitmongkol M., Vaeteewoottacharn K.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA
unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AF548023; AAO16240.1; -; Genomic_DNA. GO:0005622; C:intracellular; IEA. GO:0003700; F:transcription factor action of transcription for transcription for transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of transcription of tra
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PF00527; E7; 1
ER 65 (
   papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                           CDSTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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llarity 69.1%;
Conservative 1
                                                                  integrated into UniProtKB/TrEMBL. sequence version 1. entry version 17.
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                                                                                                                                                                                                          PRELIMINARY;
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Pred. No. 2.2e-32;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of transcription,
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Pred. No. 5.4e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor activity; IEA.
transcription, DNA-dependent;
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7_HPV33
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01-JAN-1988,
07-FEB-2006,
Protein E7.
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P06429;
                                                                                                                                                                              Snijders P.J.F., van den Brule A.J.C., Schrijnemakers H.F.J., Raaphorst P.M.C., Meijer C.J.L.M., Walboomers J.M.M.; "Human papillomavirus type 33 in a tonsillar carcinoma genera putative E7 mRNA via two 86* transcript species which are ter at different early region poly(A) sites.";
J. Virol. 66:3172-3178(1992).
EMBL;
                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome organization and nucleotide sequence type 33, which is associated with cervical coursely. Virol. 58:991-995(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=86200464; PubMed=3009902;
Cole S.T., Streeck R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                              MEDLINE=92219410; PubMed=1313922;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Alphapapillomavirus.
NCBI_TaxID=37120;
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Virus Genes 17:117-121(1998).
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Pfam; PF00527; E7; 1
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GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
                       M12732;
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AAA46959.1;
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  Genomic_DNA.mRNA.
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1_HPV52
VE7_HPV52
P36831;
                                    MOTIF
SEQUENCE
                                                                                                                                                                                                                                             MEDLINB=91258022; PubMed=1646174;
Takami Y., Kondoh G., Saito J., Noda K., Sudiro T.M.,
Sjahrurachman A., Warsa U.C., Yutsudo M., Hakura A.;
"Cloning and characterization of human papillomavirus type 52
"Cloning and characterization of human papillomavirus type 52
cervical carcinoma in Indonesia.";
Int. J. Cancer 48:516-522 (1991)
-1- FUNCTION: E7 protein has both transforming and trans-active
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PIR; A03689; W7WL33.
InterPro; IPR000118; Papvi_E7.
Pfam; PP00527; E7; 1.
DNA-binding; Early protein; Oncogene;
Transcription regulation.
CHAIN
Protein E
                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein E7.
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07-FEB-2006,
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                                                                                      Transcription regulation. CHAIN 1 99
                                                                                                                                                           EMBL; X74481; CAA52586.1; -; Genomic_DNA.
                                                                                                                                                                                                                    "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=94265501; PubMed=8205838;
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Score 295; DB 1; Ler
Score 295; DB 1; Ler
Score 295;
                                    Protein E7.

/FTId=PRO 0000133448.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.

55CFA02E4D6FE96F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-XX-C motif-1.
C-XX-C motif-2.
  Score 294; DB 1;
Pred. No. 2.2e-26;
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            Length 99;
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RESULT 41
VE7_HPV58
ID VE7_HPV58
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01-AUG-1992, sequence versi
07-FEB-2006, entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are degraded by the ubiquitin system. Direct evaluation at the N-terminal residue.";
J. Biol. Chem. 279:41414-41421(2004).
-!- FUNCTION: E7 protein has both transforming
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The tumor suppressor protein p16(INK4a) and the human papillomavirus oncoprotein-58 E7 are naturally occurring lysine-less proteins that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=15254040; DOI=10.1074
Ben-Saadon R., Fajerman I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UBIQUITINATION SITE MET-1.
PubMed=15254040; DOI=10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92024102; PubMed=1656594;
Kirii Y., Iwamoto S., Matsukura T.;
"Human papillomavirus type 58 DNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphapapillomavirus.
NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 5
Viruses; dsDNA viruses, no
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DNA-binding; Early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteasomal degradation (by host).
-!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ciechanover A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 185:424-427(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation;
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                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; D90400; BAA31846.1; -; Genomic_DNA. F36779; W7WL58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                     Similarity
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KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
                                                                      MRGNNPTLREYILDLHPEPTDLFCYEQLCDSSDEDEIGLDGPDGQAQPATANYYIVTCCY
                                                                                                               WHGDTPTLHEYMLDLOPETTDLYXXXXQLNDSSEEED-EIDGPAGQAEPDRAHYNIVTFCC
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I., Ziv T., Hellman U.,
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                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene; Transcription,
                                                                                                                                                             Score 289.5;
Pred. No. 7.2e
L6; Mismatches
                                                                                                                                                                                                                                                         Peptide (Met-Gly) (interchain with in ubiquitin) (by host). D719984F3CF48D12 CRC64;
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C-XX-C motif-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                    conjugation.
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                                                                                                                                                             .2e-26;
nes 25;
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Q547M4_HPV58
Q547M4;
24-MAY-2005,
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07-FEB-2006,
E7 protein.
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O9CCZI;
O1-MAY-2000, integrated into Unil
O1-MAY-2000, sequence version 1.
O7-FEB-2006, entry version 17.
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GO; GO:00
SEQUENCE
NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-1, E
E6/E7-HK-16;
                                                                                                                                                                                                                                 Human papillomavirus type 58. Viruses; dsDNA viruses, no RN Alphapapillomavirus. NCBI_TaxID=10598;
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                                                                                                                                        STRAIN=E7-HK-2;
Chan P.K.S., Lam C.W.,
                                                                                              Submitted
                                                                                                                    Cheng A.F.;
                                                                                                                                                                                                                                                                                                                                  E7 protein
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                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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L; AF478134; AAL85385.1; -; Genomic_DNA.
L; AF478134; AAL85388.1; -; Genomic_DNA.
L; AF478136; AAL85381.1; -; Genomic_DNA.
CG:0005622; C:intracellular; IEA.
GG:0003700; F:transcription factor activity; IEA.
GG:0006355; P:regulation of transcription, DNA-dependent;
GG:0006378; P:regulation of transcription, DNA-dependent;
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o RNA stage;
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Pred. No. 7.2e-26;
6; Mismatches 25;
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                                                                                                                                          Li W.W.H.,
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EMBL; AF478132; AAL65377.1; -; Genomic DNA.
EMBL; AF478142; AAL65387.1; -; Genomic DNA.
EMBL; AF478146; AAL65391.1; -; Genomic DNA.
EMBL; AF478147; AAL65392.1; -; Genomic DNA.
EMBL; AF478147; AAL65390.1; -; Genomic DNA.
EMBL; AF478145; AAL65390.1; -; Genomic DNA.
EMBL; AF478145; AAL65390.1; -; Genomic DNA.
EMBL; AF478145; AAL65390.1; -; Genomic DNA.
GO; GO:0005622; C:intraccilular; IEA.
GO; GO:0005625; P:regulation factor activity; IE
GO; GO:0006355; P:regulation of transcription, DNA-
InterPro; IPR000148; Papvi_E7.
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QBQSFO I
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                                                                                                                                                  EMBL;
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STRAIN=E6/E7-HK-6; PubMed=12189229; DOI=10.1093/jnci/94.16.1249; MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan l Cheung J.L.K., Cheng A.F.; Cheung J.L.K., Cheng A.F.; "Association of human papillomavirus type 58 variant with the r "Association of human papillomavirus type 58 variant with the recervical cancer.";
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Pfam; PFOC
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                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus ty Viruses; dsDNA viruses, Alphapapillomavirus.
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                                                             SEQUENCE
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                                                                            Pfam;
                                                         L; AF478139; AAL85384.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity;
GO:0006355; P:regulation of transcription, DR
erPro; IPR00148; Papvi_E7.
m; PF00527; E7; 1.
m; PF00527; E7; 1.
UENCE 98 AA; 10833 MW; 8248DD5321354CC9 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00527;
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 17;
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Score 286.5; DB:
Pred. No. 1.6e-25
7; Mismatches 21
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Pred. No. 9.4
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RESULT 45
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  RESULT 46
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ID QQQHQZ_HPV58
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AC QQQHQZ_I
DT 01-UN-2
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Matches
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Q80H02;
01-JUN-2002, integrated into
01-JUN-2002, sequence version
07-FEB-2006, entry version 1
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QBQHN7;
01-JUN-2002,
NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-17, and E6/E7-HK-18;
STRAIN=E6/E7-HK-17, and E6/E7-HK-18;
MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan
                                                                                                                                                      Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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EMBL; AF478135; AAL85380.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
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MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan i
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58 variant with the x:
cervical cancer.";
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                                                                                                                        NCBI_TaxID=10598
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GO:0006355; P:regulation of transcription, DNA-dependent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEED-EIDGPAGQAEPDRAHYNIVTFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000148; Papvi_E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.2%;
ilarity 57.1%;
Conservative 1
                                                                                                                                                                                                                                                                                      integrated into UniProtKB/TrEMBL sequence version 1.
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                                                                                                                                                                                   RNA stage; Papillomaviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 285.5; DB 2;
Pred. No. 2.1e-25;
5; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                    PRT;
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        Chan M.Y.M.,
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Best Local Similarity
                         Query Match
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:72_HPV58
Q9QC22;HPV58
Q9QC22;
01-MAY-2000,
01-MAY-2000,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=E6/E7-HK-2, and E6/E7-HK-6;
MEDLINE=22176796; PubMed=12189229; DOI=10.109
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H.
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheung J.L.K., Cheng A.F.;

"Association of human papillomavirus type cervical cancer.";

J. Natl. Cancer Inst. 94:1249-1253 (2002).
                                                                                                                                             EMBL; AF192269; AAF13690.1; -; Genomic_DNA.
EMBL; AF478133; AAL65378.1; -; Genomic_DNA.
EMBL; AF478137; AAL65382.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation_of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type S
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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EMBL; AF478149; AAL85394.1; -; Genomic_DNA.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent;

InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; 1.
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheng A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=E7-HK-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10598;
                                                                       InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10861 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/TrEMBL
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56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
  Score
Pred.
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Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                            ED3C57B911355721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stage; Papillomaviridae;
     284.5; DB 2;
No. 2.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOI=10.1093/jnci/94.16.1249;
Li W.W.H., Lo K.W.K., Chan
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                                                                            CRC64;
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                            Length
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RESULT 49
Q80SE8 HPV58
ID Q80SE8;
AC Q80SE8;
DT 01-UUN-2002;
DT 07-FEB-2006;
DT 07-FEB-2006;
DE E7 protein.
OS Human papillon
OC Viruses; dsDN/
OC Alphapapillon
OX NCBI_TaxID=100;
RN [1]
RN NUCLEOTIDE SEC
RC STRAIN=E6/E7-1-
RX MEDLINE=221767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 48
QROSES HYVES
ID OROSES HYVES
AC OROSES TO 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
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DT 01-JUN-2
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DT 07-FEB-2
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 NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-13;
MEDLINE=22176796; Pu
                                                                                             Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                 01-JUN-2002, integrated into U01-JUN-2002, sequence version 07-FEB-2006, entry version 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002, integrated into u
01-JUN-2002, sequence version
07-FEB-2006, entry version 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Cheng A.F.; Tassociation of human papillomavirus type 58 variant with the risk of cervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 58.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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QBQSE9;
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Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10833 MW;
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GG:0005622; G:intracellular; IEA.
GO:0003700; F:trangcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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                                                                                                                                                                                                                                                                                                                                                                             KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.8%;
                                                                                                              type 58.
es, no RNA
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Pred. No. 3.7e-25;
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01-MAY-2000, integrace version 01-MAY-2000, sequence version 01-MAY-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Human papillomavirus type 6vc;
MEDLINE=99429608; PubMed=10501500;
Kovelman R., Biter G.K., Roman A., Brown D.R., Barbosa M.S.;
"Human papillomavirus type 6: classification of clinical isol
functional analysis of E2 proteins.";
J. Gen. Virol. 80:2445-2451(1999).
                                                                                                                                                                                                                                                 EMBL; AF092932; AAF00065.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, Dt
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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NCBI_TaxID=31552;
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"Association of human papillomavirus type 58 vacervical cancer.";
J. Natl. Cancer Inst. 94:1249-1253(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus
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GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DN
InterPro; IPR000148; Papvi_E7.
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                                                                                                     MHGDTPTLHEYMLDLQ-PETTDLYXYXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC
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CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK
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                                     CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
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                                                                                                                                                       Score 247; DB
Pred. No. 7.3e
14; Mismatches
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Pred. No. 6.
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7.3e-21;
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VET HYV11

ID VET HYV11

ID VET HYV11

ID PO402

AC P0402

AC P1402

  RESULT
VE7_HPV
ID - VE
AC PC
DT 01
DT 01
DT 07
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                                                                                                                                                                                                                                    ULT 52
HPV6B
                                                                                                                  VE7 HPV6B
P06464;
01-JAN-1988,
01-JAN-1988,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VE7 HPV11 STANDARD,
P04020;
23-OCT-1986, integrated into UniProtKB/Swiss-Prot.
23-OCT-1986, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].

Fife K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;

Fise K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;

"Association of human papillomavirus 11 DNA with squamon carcinoma of the tongue.";

Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                        Protein E7.
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M14119; AAA46928.1; -; Genomic_DNA.
EMBL; L36108; AAA21704.1; -; Genomic_DNA.
PIR; A03690; W7WL11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The nucleotide sequence and genome virus type 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activities.
-!- SIMILARITY: Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00527; E7;
DNA-binding; Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dartmann K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (GENOMIC DNA).
MEDLINE=86181601; PubMed=3008427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHGDTPTLHEYMLDLQ-PETTDLYXYXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC
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                                                                                                                                                                                                                                                                                                                                                      CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                          MHGRIVTLKDIVLDIQPPDPVGLHCYEQLEDSSEDEVDKVD--KQDAQPLTQHYQILTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                  integrated into UniProtKB/Swiss-Prot. sequence version 1. entry version 37.
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91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation.
                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.4%;
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94
                          es, no
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                        RNA stage; Papillomaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein E7.
/FTId=PRO_0000133410.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 1.3e-20;
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                                                                                                                                                                                                                86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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RESULT 53
VE7_HPV6A
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Best Local S
Matches 52
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                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (GENOMIC DNA).

MEDLINE=95297152; PubMed=7778283;

Hofmann K.J., Cook J.C., Joyce J.G., Brown D.R., Schul-
George H.A., Rosolowsky M., Fife K.H., Jansen K.U.;

"Sequence determination of human papillomavirus type 6.

"Sequence determination in Saccharomyces cerevisiae.";

"Of virus-like particles in Saccharomyces cerevisiae.";

Virology 209:506-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VE7_HPV6A
Q84292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 6b.
EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998, integrated into UniProtKB/Swiss-Prot. 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 30.
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Pfam; PF00527; E7; 1.
DNA-binding; Early protein; On
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MEDLINB=84131949; PubMed=6321162;
MEDLINB=84131949; PubMed=6321162;
Schwarz E., Durst M., Demankowski C., Lattermann
Schwarz E., Suhai S., Zur Hausen H.;
"DNA sequence and genome organization of genital
Pfam; PF00527
DNA-binding;
                                                                  EMBL; L41216; AAA74212.1; -; Genomic
                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                              -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein E7.
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-!- SIMILARITY: Belongs to
                                               InterPro;
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                                               IPR000148;
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llarity 52.5%;
Conservative 1
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94
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  protein; Oncogene; Transcription;
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                                        Papvi_E7.
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/FTId=PRO_
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                      see http://www.uniprot
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1.2e-20;
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                                                                                                                                                                                                                                and trans-activating
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RESULT

VE7-HPV

ID 7 O11

DT 011

DT 
RESULT 55
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Best Local S
Matches 48
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Best Local (
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7 HPV34

VE7 HPV34

P36828;

01-JUN-1994;
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MOTIF
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Early protein; Oncogene; Transcription; Transcription regulation.

1 97 Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delius H., Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=333764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ram;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; X74476; CAA52556.1; -; Genomic_DNA.
S36516; S36516.
EPCO; IPRO00148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00527; E7; 1.
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                                                                                            RCQSTVCLTIESTHADLLVLEDLLMGALKIVCPNCSRR 96
                                                                                                                                   KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCDSNVRLVVQCTETDIREVQQLLLGTLDIVCPICAPK 97
                                                                                                                                                                                 MHGKKPSVQDIVLDLKPTTETDLTCYESL-DNSEDEDETDSHL-ERQAEQAWYRIVTDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC
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90
7 AA;
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o RNA stage;
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                                                                                                                                                                                                                                                                      Score 222.5; DB 1;
Pred. No. 5.5e-18;
8; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                              /FTId=PRO_0000133432
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 242; DB 1;
Pred. No. 2.8e-20;
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/FTId=PRO_0000133404.

C-XX-C motif-1.

C-XX-C motif-2.
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RESULT 56
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ID Q91194 HPV16
AC Q91194;
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Best Local Similarity
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Best Local
                      Query Match
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DN
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Zhao M., Wu X.X., Ding X.H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001, integrated into UniProtKB/TrEMBL 01-DEC-2001, sequence version 1. 07-FBB-2006, entry version 12. Truncated E7 protein.
                                                                       SEQUENCE
                                                                                                                                        EMBL, AF393782; AAK84003.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terai M., Burk R.D.;
"Identification and characterization of 3 novel genital human papillomaviruses by overlapping polymerase chain reaction: candHPV89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transforming protein Human papillomavirus - cand90. Viruses; dSDNA viruses, no RNA Alphapapillomavirus.
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01-OCT-2002, sequence version
07-FEB-2006, entry version 11
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Q8JNAO;
                                                                                                                    InterPro;
                                                                                                                                                                                                                                                               Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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MEDLINE=22079881; PubMed=12085327; DOI=10.1086/340824;
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=333769;
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                                                                                                PF00527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MHGDTPTLHEYMLDL-QPETTDLYXYXQLNDSSEEEDEIDG--PAGQAEPDRAHYNIVTF
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45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGQRPTLKDIFLELDQPDAVDLHCNEQLASSEEEDNREDGEQPTQPTEPAQQAYRVVTS
                                                                                                                    IPR000148;
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Dis. 185:1794-1797(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                         E7;
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                                                                1.
4903 MW;
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42.7%;
95.3%;
                                                                                                                    Papvi_E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no RNA stage; Papillomaviridae;
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Score
Pred.
                                                                       19A57D4E52FB14D6 CRC64;
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Pred. No. 7.
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221;
No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
  .; DB 2;
3.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4e-18;
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                                                                                                                                          DNA-dependent;
                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                      IEA.
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                           43;
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RESULT 58

Q9WHG1 9PAPI
ID Q9WHG1,
AC Q9WHG1;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-EBB-2006, entry version 17.
DE Putative transforming protein E7.
OS Human papillomavirus - cand85.
OC Viruses; daDNA viruses, no RNA stage; Papillomav OC Alphapapillomavirus.
OX NCBI TaxID-151757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 57
VET PAIN
ID VET R
AC P2216
AC P2216
AC P2216
DT 01-AU
DT 01-PE
DE Prote
GN Name=
OS Rhesu
OC Virus
OC Alpha
OX NCB1
RN NCB1
RN NCB1
RN NCB1
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Best Local S
Matches 49
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P22161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60184; AAA79312.1; -; Genomic_DNA.
PIR; B38503; W7WLR1.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ostrow R.S., Labresh K.V., Faras A.J.;
"Characterization of the complete RhPV 1 genomic sequence integration locus from a metastatic tumor.";
Virology 181:424-429(1991).
-i- FUNCTION: E7 protein has both transforming and trans-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus papillomavirus type
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=91135018; PubMed=1847267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                        13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDL----QPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                        PEDGDCYRIVSDCYSCGKPLRLVVVSSHEELRVLEDLLMGTLDIVCPSCASR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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106
113 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence version 1. entry version 32.
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109
12818
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43.8%; Pred. No. 2e-
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RNA stage;
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/FTId=PRO 0000133470.

C-XX-C motif-1.

C-XX-C motif-2.
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3; Mismatches
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                                                                                                      Papillomaviridae;
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RESULT
VE7_HPV
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VE7 HPV45
P21736;
01-MAY-1991,
01-JUN-1994,
07-FEB-2006,
Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF131950; AAD24182.1; -; Genomic_DNA. GO; GO:0005622; C:intracellular; IEA. GO; GO:0003700; F:transcription factor activity; IEA. GO; GO:0003700; F:transcription of transcription, DNA-dependent; GO; GO:006355; P:regulation of transcription, DNA-dependent; IRCETPO; IPRO00148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chow V.T., Leong P.W.; "Complete nucleotide sequence, genomic organization and phylogenetic "Complete nucleotide sequence, genomic organization and phylogenetic analysis of a novel genital human papillomavirus type, HLT7474-S."; J. Gen. Virol. 80:2923-2929(1999).
            Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN
                                                                      EMBL; X74479; CAA52574.1; -; Genomic_DNA.
EMBL; M38198; AAA46974.1; -; Genomic_DNA.
PIR; S36562. S36562.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                    Kaplan J.B., Burk R.D.,
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: E7 protein has both transforming and trans
                                                                                                                                                                                                                                                                                       Delius H., Hofmann B.; "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chow V.T.K., Leong W.F.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20047972; PubMed=10580054;
                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10593;
                                                                                                                                                                                          -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence version
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Best Local S
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GO; GO:00
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Name=HPV45 E7;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini; Homini
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CONFLICT
CONFLICT
SEQUENCE
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Sastre-Garau X., Favre M., Couturier J., Orth G.;

"Distinct patterns of alteration of myc genes associated with integration of human papillomavirus type 16 oe type 45 in two
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000148; Papvi_E7. Pfam; PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Favre M.
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Q9Y4Y3;
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01-NOV-1999, sequence version
07-FEB-2006, entry version 12
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G0:0005622; C:intracellular; IEA.
G0:0003700; P:transcription factor activity; IEA.
G0:0006355; P:regulation of transcription, DNA-dependent;
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43.8%; Pred. No. 1.1e-16;
tive 15; Mismatches 32
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C-XX-C motif-2.

G -> E (in Ref. 2).

R -> Q (in Ref. 2).

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Terai M., Burk R.D.;
Submitted (OCT-2001) to
    SEQUENCE
                                                                    EMBL; AF436130; AAO15456.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                  Viruses, dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003, sequence version 07-FEB-2006, entry version
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GO; GO:0003700; F:transcription factor activit;
GO; GO:0006355; P:regulation of transcription,
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NCBI_TaxID=10593;
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Viruses; dsDNA viruses, no RN
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                           Pro; IPR000148; Papvi_E7. PF00527; E7; 1.
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Viruses, dsDNA viruses,
                       Protein E7.
Name=E7;
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CHAIN 1 105 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primer-directed sequencing of human papillomavirus types.", Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-I- FUNCTION: E7 protein has both transforming and trans-act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA] MEDLINE=94265501; PubMed=8205838;
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-!- SIMILARITY: Belongs to the papillomaviruses E7
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S36504; S36504.
papillomavirus
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                                                                                                                                                                                                                                                                                                       IVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                          MHGKVTTIPEYILDLVPQTEIDLHCYEQLNSSEEEDEDEVDNLQKQPQQARQEEQHPCYL
                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEE-EDEIDG----PAGQAEPDRAH--YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNRSLRLVVQCTGPDINNLHTLLLGTLSLVCPLCAPK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGKYPTLKEIVLQLQPDPVGLLCNEQLDSSEEEVDEL---ATQATQHTQPYQIVTCCCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000148; Papvi_E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
98
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                            integrated into UniProtKB/Swiss-Prot. sequence version 1. entry version 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence version entry version 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽,
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
101
12001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            es, no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein E7.

/FTIG=PRO 0000133428.

C-XX-C motif=1.

C-XX-C motif=2.

C-XX-C motif=2.

M; 6166758B14B44D67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 209.5; DB 1; Length Pred. No. 2.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1e-16;
ches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105;
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                                                                                                                                                                                                                                                                                                                                                                                                      53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                          056947_9PAPI
056947_9PAPI
056947;
                                                                                                                                                        NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=98118461; PubMed=9454709; DOI=10.1006/viro.1997.8943;
Delius H., Saegling B., Bergmann K., Shamanin V., de Villiers
The genomes of three of four novel HPV types, defined by dif
                                                                                                                                                                                                                                                                                                   01-JUN-1998, integrated into UniProtKB/TrEMBL 01-JUN-1998, sequence version 1. 07-FEB-2006, entry version 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                    Alphapapillomavirus.
NCBI_TaxID=69986;
                                                                                                                                                                                                                                                                 Human papillomavirus type 7 Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                        E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               una-binding; Early protein;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333765;
  SEQUENCE
                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delius H., Hofmann B.;
                                                                                                                                       Virology 240:359-365(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr. Top. Microbio1. 1mn
-!- FUNCTION: E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                  L; Y15175; CAA75464.1; -; Genomic DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity
GO:0006355; P:regulation of transcription,
GO:0006355; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S36528; S36528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X74482; CAA52592.1; -; Genomic
              PF00527;
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45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
                                                                                                                                                                                                                                                                                                                                                                                                                     IETQCCRCESLVQLAVQSSTKELRILQQMLMGTVELVCPLCATR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGNVPTLPQYIIELIPQTEIDLQCHEQLNSSEDEDEDEVDHLQEQPQQARRDEQHPCYL
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98
105 AA;
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1.
9971 MW;
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12162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        has both transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₩;
                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                  RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein E7.
/FTId=PRO 00001
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 208.5; DB 1;
Pred. No. 2.7e-16;
3; Mismatches 29;
  ABAB4EADABACF33B CRC64
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                 stage; Papillomaviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEA7E2E8D0C1F7EC
                                                 factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA.
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                                    DNA-dependent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                    IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                           Villiers E.M.;
ed by differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                       IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Query Match

Score 207.5;

DB 2;

Length

90;

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Q82006 HPV73
ID Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
AC Q82006;
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AC Q82006;
AC Q8206;
ULT
Q6EGQ8
ID Q6EGQ8
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DT 16
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COC VI
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Best Local 9
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Viruses; dsDNA viruse
Alphapapillomavirus.
NCBI TaxID=120686;
                                                                                                                                                          16-AUG-2004,
16-AUG-2004,
07-FEB-2006,
                                                                                                                                                                                                                                             Q8_9PAPI
Q6EGQ8_9PAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLECTIDE SEQUENCE.

MEDLINE=96213783; PubMed=8635859;

DOI=10.1002/(SICI)1097-0215(19960516)66:4<453::AID-IJC7>3.0.CO;2-V;

Voelter C., He Y., Delius H., Roy-Burman A., Greenspan J.S.,

Greenspan D., de Villiers E.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94165; CAA63883.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 73.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q82006_HPV73
Q82006;
                                                                                                                                                                                                                               Q6EGQ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006, entry version 20 E7 protein.
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                                                                                       Human papillomavirus type 71.
                                                                                                                  Name=E7;
                                                                                                                                     Putative transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=51033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Int. J. Cancer 66:453-456(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPV types present in oral papillomatous [V infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ы
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                                                                  deDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEBEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSSTLRLVVESSEADIRAFQELLLRTLKIVCPRCA
                                                                                                                                                                                                                                                                                                                                                                      KCQCTVCLAIESNKADLRVIEELLMGTLGIVCPNCSR
                                                                                                                                                                                                                                                                                                                                                                                                                 KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGKKTTLQDITLDLKPTTEIDLTCYESL-DNSEDEDETDSHLDR-QAERECYRIVTDCT
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                                                                                                                                                            sequence version entry version 13
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                                                                  RNA stage;
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Pred. No. 3.7
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                                                                  Papillomaviridae;
                                                                                                                                                                                                                                                       94
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  Best Local Similarity
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RESULT 68
Q2VJC6 9PAPI
ID Q2VJC6,
AC Q2VJC6,
DT 10-JAN-2
DT 10-JAN-2
DT 07-FEB-2
DE E7 protect
OS Human pa
OC Viruses;
OC Alphapas;
OC Alphapas;
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AN ILI
TR NUCLEOTI
RC STRAIN-C
RX PUBMEd=1
RA NARCHARIN-C
RX PAPAILON
RA J, Virol
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CC Distrib
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SEQUENCI
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QZVJC6;
                                                                              EMBL; DQ080082; AAZ39514.1; -; SEQUENCE 95 AA; 10541 MW; I
                                                                                                                                                                                                                                         PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510. Narechania A., Chen Z., Desalle R., Burk R.D.; "Phylogenetic Incongruence among Oncogenic Genital Papillomaviruses."; J. Virol. 79:15503-15510(2005).
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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EMMBL; AY330623; AAQ95199.1; -; Genomic_DNA.
EMBL; AY330620; AAQ95178.1; -; Genomic_DNA.
EMBL; AY330620; AAQ95178.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity
GO; GO:00003755; P:regulation of transcription,
                                                                                                                                                                Distributed
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Pfam; PF00527; E7; 1.
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ction of HPV71
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                                                                                                                                                          by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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39.8%;
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Score 206; DB 2;
Pred. No. 4.7e-16;
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                                                                                 FDD5E210EE230741
                                                                                                             Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stage; Papillomaviridae;
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cogenic Genital Alpha
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Matches 46
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7_HPV29
VE7_HPV29
P50784;
01-OCT-1996,
07-FEB-2006,
                                                                          ULT 70
HPV18
VE7 HPV18
P06788;
Human papillomavirus type
Viruses; dsDNA viruses, n
Alphapapillomavirus.
NCBI_TaxID=333761;
                                     01-JAN-1988,
01-APR-1990,
07-FEB-2006,
Protein E7.
Name=E7;
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MOTIF
SEQUENCE
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the papillomaviruses E7
                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 29.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein E7.
                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                       EMBL; U31784; AAA79430.1; -;
                                                                                                                                                                                                                                                                                                                                                                                       Alphapapillomavirus.
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                                                                                                                                                                                                                                                        Transcription
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=37112;
                                                                                                                                                                                                                                                              NA-binding, Early
                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                           FUNCTION: E7
                                                                                                                                                                                                                                                                                                                                  activities.
                                                                                                                                                                                                                                                                       PF00527; E7;
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                                                                                                                                                                                    46;
                                                                                                                                                                                          Similarity
                                                                                                                       CSTTLRLVVESSEADIRAFQELLLRTLKIVCPRCA 90
                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEDDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCGRAVRLVVESGHAELRVLQELLLGALGIVCPHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
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                                                           integrated into UniProtKB/Swiss-Prot sequence version 2.
                                                    entry
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86
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                                                                                                                                                                                                                                                       regulation.
                                                                                  STANDARD;
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                                                     version
                                                                                                                                                                                                                  9971 MW;
                                                                                                                                                                                                                                                               protein; Oncogene; Transcription;
                                                                                                                                                                                          39.6%;
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6
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                             type
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                      18.
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                                                                                                                                                                                     12;
                                                                                                                                                                                   Score 204.5;
Pred. No. 6.7e
L2; Mismatches
                                                                                                                                                                                                                         Protein E7.
/FTId=PRO 00001
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                     Genomic_DNA.
                                                                                                                                                                                                                  2DFA0BA85E4CE6CE CRC64;
                                                                                  PRT;
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                       stage;
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                                                                                                                                                                                    6.7e-16;
ches 32;
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                      Papillomaviridae;
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RESULT 71
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ID Q6EPGP1 HUMAN
AC Q6EPGP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05015; CAA28665.1; -; Genomic_DNA.
EMBL; M20324; AAA99513.1; -; mRNA.
EMBL; M20325; AAA99515.1; -; mRNA.
EMBL; M26798; AAA46947.1; -; Genomic_DNA.
EMBL; X04773; CAA28467.1; -; Genomic_DNA.
EMBL; A06324; CAA00540.1; -; Unassigned_DNA.
EMBL; A06328; CAA00543.1; -; Unassigned_RNA.
EMBL; B06328; CAA00543.1; -; Unassigned_RNA.
EMBL; B06328; CAA00543.1; -; Unassigned_RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=88188247; PubMed=2833614;
Inagaki Y., Tsunokawa Y., Takebe !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tupistributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=87218459; PubMed=3034571;
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transcription patterns of human
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"Different human cervical carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA] . MEDLINE=87053870; PubMed=3023067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequences of cDNAs for transcripts in HeLa cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=87283882; PubMed=3039146;
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DNA-binding; Early protein;
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42; Conserv
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HTMLCMCCKCEARIKLVVESSADDLRAFQQLFLNTLSFVCPWCASQ
                       YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXFICSQK::: | | | | : | : | : | : | | | | | : :
                                                                                                                         WHGDTPTLHEYMLDLOPET---TDLYXXXXQLNDSSEEEDEIDG----PAGQAEPDRAH
                                                                                    MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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98
73
105 AA;
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C-XX-C motif-1.
C-XX-C motif-2.
C-XX-C motif-2.
K -> E (in Ref. 1 and 4).
W; 2CDB119534D0186A CRC64;
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                                                                                                                                                                                          Pred.
                                                                                                                                                                                                         Score 202.5;
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illomavirus type 18 earl
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ches 32;
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PRELIMINARY; integrated into

UniProtKB/TrEMBL

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RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Scapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bonak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA RACkinger A.C., Grimwood J., Schmutz J., Myers R.M.,
RA RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                   2SULT 72
7 HPV13
0 VE7 HPV13
002271;
01-APR-1993,
01-APR-1993,
07-FEB-2006,
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                 Protein E7.
Name=E7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004, sequence version 07-FEB-2006, entry version 10. Hypothetical protein. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000148; Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L; BC056907; AAH56907.1; -; mRNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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papillomavirus
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                                                     sequence version entry version 33.
                                                                                            integrated into UniProtKB/Swiss-Prot
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type
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Pred. No. 1.4e
21; Mismatches
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RESULT 73
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Matches 46
                                                                                                                 PubMed=16306621; DOI=10.1128
Narechania A., Chen Z., Desa
"Phylogenetic Incongruence a
Papillomaviruses";
J. Virol. 79:15503-15510(200
                                                                                                                                                                                                                                                                    10-MAY-2005,
10-MAY-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOTIF
SEQUENCE
                   "Small tumor virus genomes are int attachment regions in transformed J. Virol. 75:12339-12346(2001).
                                                       MEDLINE=21568387; PubMed=11711624;
DOI=10.1128/JVI.75.24.12339-12346.2001;
Shera K.A., Shera C.A., McDougall J.K.;
                                                                                                                                  NUCLEOTIDE SEQUENCE.
PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
Narechania A., Theongruence among Oncogenic Genital Alpha
                                                                                                                                                                                                            Human papillomavirus
Viruses; dsDNA viruse
Alphapapillomavirus.
                                                                                                                                                                                                                                                   Name=E7;
                                                                                                                                                                                                                                                                                                          Q76Z96;
                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                 NCBI_TaxID=333761;
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PIR; B42955; W7WL13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human papillomavirus type 13 and pygmy chimpanzee 1: comparison of the genome organizations."; Virology 190:587-596(1922).
-1- FUNCTION: E7 protein has both transforming and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=92391075; PubMed=1325697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed
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NCBI_TaxID=10573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rram;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   !- SIMILARITY: Belongs to the papillomaviruses
                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pro; IPR000148;
PF00527; E7; 1
                                                                                                                                                                                                                                                                                                                                                                               58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                          dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                               LTSCSKCCSNVRLVVECTGPDIHDLHDLLLGTLNIVCPLCAPK 100
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                                                                                                                                                                                                                                                                                                                                                                                                     VTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
                                                                                                                                                                                                                                                                                                                                                                                                                             WHGKYPTLKDIVLELTPDPVGLHCNEQLDSS---EDEVDEQATQATQATQHSTLLQCYQI
                                                                                                                   79:15503-15510(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA;
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by the
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94
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.8%;
                                                                                                                                                                                                                                    type
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                                                                                                                                                                                                                            RNA
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Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 200.5;
Pred. No. 2.3
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C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                              UniProtKB/TrEMBL
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                                   integrated
med cells."
                                                                                                                                                                                                                         stage; Papillomaviridae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ches 35;
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                                              near nuclear
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                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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RESULT 74
QGEGQ1 9PA
ID EGGQ1
QGEGQ
AC QGEGQ
AC QGEGQ
DT 16-AI
DT 07-F
DT 07-F
DE PUTA
OC Huma
OC Viru
OC Alpi
OX NCB:
RN (1)
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RESULT 75
Q9QNP7 HPV
Q9QNP1
ID Q9QNI
AC Q9QNI
DT 01-M2
DT 01-M2
DT 07-F1
DE E7 p1
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Best Local S
Matches 41
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Best Local S
Matches 42
1P7_HPV18

Q9QNP7_HPV18

Q9QNP7;

Q1-MAY-2000,

Q1-MAY-2000,

Q7-FEB-2006,

E7_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QĞEGQ1_9PAPI PRELIMINARY;
QĞEGQ1;
16-AUG-2004, integrated int
16-AUG-2004, sequence versi
07-FEB-2006, entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY262282; AAP20595.1; -; Genomic_DNA.
EMBL; AF339139; AAL34458.1; -; Genomic_DNA.
GO; GO:0005622; C:intraccellular; IEA.
GO; GO:0003700; F:transcription factor activity
GO; GO:0006355; P:regulation of transcription,
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.58
88.68
88.88
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphapapillomavirus.
NCBI_TaxID=120686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative transforming protein E7. Human papillomavirus type 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; B7; 1.
SEQUENCE 94 AA; 10499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-de
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                                                                                                                                                                                                                                                                                                                                                                                                       1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                     MRGQQCTLKDIVLQLQPEVVDLYCHEQFASSDEGDNRVDGEQ-PTEPAQQAYRVVSYCGR 59
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P
                                                                                                                           PRELIMINARY;
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39.6%; Pred. No. 2.4e-15;
tive 20; Mismatches 33
                                                       version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no RNA stage;
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Pred. No. 2.7e-15;
5; Mismatches 37;
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transcription, DNA-dependent;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
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                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=89259065; PubMed=2542593;
MEDLINE=89259065; PubMed=2542593;
MEDLINE=89259065; PubMed=2542593;
                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                      NUCLEOTIDE SEQUENCE. de Villiers E.M.;
                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Matsukura T., Delius
Submitted (JAN-2004)
                                                                                                                                                                                                                                                                                                                          "Cloning and partial DNA sequencing of two new types associated with condylomas and low-grade J. Virol. 63:2829-2834(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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                                                                                                                          Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00527; E7; 1.
NCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;
     AJ620205;
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     CAF05784.1; -;
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                                                                                                                                                                                                                               , Sugase M.;
the EMBL/Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage; Papillomaviridae;
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Pred. No. 4.1
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  Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt B.
                                                                                                                                                                                                                                                                                                                                                      human papillomavirus cervical neoplasia.";
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RESULT 78
Q81965 HPV59
ID Q81965 HPV59
AC Q81965;
DT 01-NOV-1996;
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Best Local
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OSONP6;
O1-MAY-2000, integrated into 1
O1-MAY-2000, sequence version
O7-FEB-2006, entry version 14
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GO; GO:0003700; F:transcription facto
GO; GO:0006355; P:regulation of trans
InterPro; IPR00148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 99 AA; 11187 MW; CAE98EA
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                                                                                                                                                                                                                                                                                                          NUCLEOTIDE
Veiko V.P.
                                                                                                                                                                                                                                                                                                                                Virus
[2]
                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Laassri M., Gul'ko L.,
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Viruses; dsDNA viruses, no RN
                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=333761;
                                                                                                                                                                                                                                                                                                                                                                                                                   Alphapapillomavirus.
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GG:0005622; C:intracellular; IEA.
GC:00003700; F-transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-de
erPro; IPRO00148; Papvi_E7.
m; PPF00527; E7; 1.
UENCE 105 AA; 12009 MW; C4979555DAD4A960 CRC64
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                                                                                                                               MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCLCVIRLVVQCSDSDIKKLEDLLLGTLKIVCPLCT 95
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                                                                                           YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                              MHGPKATLQNIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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      integrated
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                          PRELIMINARY;
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                                                                                                                                                              38.0%; Score 196.5; 39.6%; Pred. No. 7e-
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        into
                                                                                                                                                                                                                                                                                                                                                                                                                            no RNA stage;
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Pred. No. 4.4e-1
L4; Mismatches
                                                                                                                                                              Pred. No. 7e-15;
                                                                                                                                                                                                                     of transcription, DNA-dependent;
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       UniProtKB/TrEMBL
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                          PRT;
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VE7_PCPV1
ID VE7_F
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InterPro; 1...
ofam; PF00527; E7; 1
ofam; PF00527; Early ;
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Q02272;
Q1-APR-1993,
Q1-APR-1993,
                                                    Copyrighted
Distributed
                                                                                                                                                                                                                                      Protein E7.
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                                                                                                                                          Opdenakker G.;
                                                                                                                                                                                                                                Name=E7
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                                                                                                                                                                                        NCBI_TaxID=10576;
                                                                                             activities.
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                        IPR000148; Papvi
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                                                                                                                                                                                                                                                                                        STANDARD
      protein;
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07-FEB-2006, entry version 2
ORF putative E7 protein.
Name=ORF putative E7;
Human papillomavirus type 59
Viruses; dsDNA viruses, no RI
Alphapapillomavirus.
NCBI_TaxID=37115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

MEDLINE=94303229; PubMed=8030272;

MEDLINE=94303229; PubMed=8030272;

Page Burman A., Kim H., de Villiers E.-M.,
                                                                                                                                                                                                                      "Human papillomavirus type 13 and pygmy chimpanzee 1: comparison of the genome organizations."; Virology 190:587-596(1992).
-I- FUNCTION: E7 protein has both transforming and
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MEDLINE=92391075; PubMed=1325697;
Van Ranst M., Fuse A., Fiten P., Beuken
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Ffam; PF00527; E7; 1.
SEQUENCE 107 AA; 12042 MW; A8F2B6973D727163 CRC64;
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papillomavirus type 59.";
Virology 203:158-161(1994).
                                                                 EMBL; X62844; CAA44656.1; -;
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                                                                                                                                                                            - I- SIMILARITY: Belongs to the papillomaviruses E7 protein
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RESULT 81
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Shera K.A., Shera C.A., McDougall J.K.;
"Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
J. Virol. 75:12339-12346(2001).
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/FTId=PRO 0000133464.
C-XX-C motif-1.
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55 HPV18
600NP5_HPV18 PRELIMINARY; PRT; 105 AA.
600NP5;
01-MAY-2000, integrated into UnitrotkB/TrEMBL.
01-MAY-2000, sequence version 1.
01-FEB-2006, entry version 14.
EMBL; Y184>>; ....
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; F:regulation of transcription, Di
                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                             Submitted (DEC-1998) to
                                                                                                                                                                                      NUCLEOTIDE SEQUENCE Veiko V.P.;
                                                                                                                                                                                                                                                            "Cloning of E6 and E7 Genes of Transformation Potential of E7 Virus Genes 182:139-149(1999).
                                                                                                                                                                                                                                                                                                                                 Laassri M., (
Kisseljev F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 1 Viruses; dsDNA viruses, no Alphapapillomavirus.
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Distributed under the Creative Commons Attribution-NoDerivs License
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"Cervical HPVs
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Narechania A., Chen Z., DeBalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha
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                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=333761;
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                                      Y18493; CAB53099.1; -; Genomic_DNA.
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               C:intracellular;
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                                                                                                                                                                                                                                                                                                                                                           Vinokurova S., Kisseljova N., Veiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 191.5; DB 2; ; Pred. No. 2.4e-14; 17; Mismatches 31;
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                                                                                                                                                                                                                                                                                      Gene
                                                                                                                                                                                                                                                                                                             Human Papilloma Virus Type 18
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RESULT 84
Q21283 HPV13
ID Q21283 HPV13
AC Q21283;
DT 07-MAR-2006, i
DT 07-MAR-2006, c
DT 07-MAR-2006, c
DE E7.
GN Name=E7;
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01-OCT-2002,
07-FEB-2006,
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CG7_SPAPI
QBJTG7_SPAPI
QBJTG7;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
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Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=202252;
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GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 105 AA; 11952 MW; 247BF448A6BBB4FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of 3 novel genital human papillomaviruses by overlapping polymerase chain reaction: candHPV89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=22079881; Pu
Terai M., Burk R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             candHPV90, and candHPV91.";
J. Infect. Dis. 185:1794-1797(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR000148; Papvi_E7.
PF00527; E7; 1.
                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                           KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPET---TDLYXXXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQ-AEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTMLCMCCKCEARIELVVESSADDLRAFQQLFLKTLSFVCPWCASQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                          SCYCSIRLVVKCSSSDIKTLEELLLGTLQIVCPLCT 95
                                                                                                                                                                                                                                                                                                                                                                                               MYGKEPTLRDYVLTLQPEPRSLTCDEQL-DSSDSEDEREQSTQQDQQVDLQVYKVVTECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGPKATLQDIVLHLEPQNEIPVGLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrated into t
sequence version
                                                           entry version
                                                                            sequence version
                                                                                                         integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=12085327; DOI=10.1086/340824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.
11952 MW; 247BF448A6BBB4FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cand91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ខ្ល
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 191.5; DB 2
Pred. No. 2.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 191; DB 2;
Pred. No. 2.9e-14;
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6874FAE881797E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                             98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 59
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RESULT 85
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ID Q98005 0
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                                                                                                                                                                                           Matches
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                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.

MEDLINE=963/9050; PubMed=8784613;

Longuet M., Cassonnet P., Orth G.;

"A novel genital human papillomavirus (HPV),

immunosuppressed patients.";

J. Clin. Microbiol. 34:1859-1862(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 13.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI TaxID=10573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphapapillomavirus.
NCBI_TaxID=44028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   098005_9PAPI
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Distributed
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE.
Borborema-Santos C.M.,
                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U40822; AAC55128.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amazon."
                                                                                                                                                                                                                                                                                                          InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQ344807; ABC79058.1; -; Genomic
NCE 98 AA; 10738 MW; 97D6627CE
                                             60
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                                                                                                                                                                                         45;
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                                                                                                                                                                                                                  Similarity
                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH-YNIVTFCC
                                             KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
VCNRSLRLVVQCTGPDINNLHTLLLGTLNLVCPLCAPK
                                                                                          WHGKYSTLKEIVLELQPDPVGLHCNEQLDSSEEEVDEL---ATQATQQLTQAYQIVTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
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                                                                                                                                                                                                                                                                                      96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome analysis of HPV type 13
                                                                                                                                                                                                                                                                                      10522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.8%;
45.0%;
                                                                                                                                                                                                             36.6%;
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                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                      Score 189; DB
Pred. No. 4.8e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 190; DB 2; Pred. No. 3.8e-14; 37;
                                                                                                                                                                                                                                                                                      8DF8480CEE5CCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97D6627CB7CF896D CRC64;
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                                                                                                                                                                                                                  .8e-14
                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPV type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S., Astolfi-Filho
3 isolated in the
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found
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                                                                                                                                                                                                                                                                                                                                                              IEA.
                                                                                                                                                                                         Gaps
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                                                                                            57
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RESULT 87
VE7 HPV42
ID - VE7 H
AC P2723
DT 01-AU
DT 07-FE
DE Prote
GN Name=
OS Humann
OC Virus
OC Alpha
OX NCB1
RN [1]
RN [1]
RN MUCLI
RN MEDLI
RA Phili
RA Phili
RA Phili
CC -1- |
CC -1- |
CC -1- |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VE7_HPV28
ID VE7 HPV28
AC P50783;
AC P50783;
DT 01-CCT-1996, i
DT 01-FEB-2006, e
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Best Local S
Matches 43
                                                                                                                                                                                                                                    VE7_HPV42
P27231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTIF
SEQUENCE
                               organization.";
Virology 186:331-334(1992).
-I- FUNCTION: E7 protein has both transforming
                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=92087479; PubMed=1309278;
Philipp W., Honore N., Sapp M., Col
"Human papillomavirus type 42: new
                                                                                                                          Human papillomavirus ty,
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10590;
                                                                                                                                                                                                  01-AUG-1992,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=37111;
                                                                                                                                                                                                                       01-AUG-1992, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activities.
-i- SIMILARITY: Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             Name=E7
                                                                                                                                                                                        Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000148; Papvi_E7
Pfam; PP00527; E7; 1.
DNA-binding; Early protein; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U31783; AAA79423.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 28.
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=E7
            activities.
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                          PKCSSPLRLVVECSHADIRALEQLLLGTLTVVCPRC
                                                                                                                                                                                                                                                                                                                     CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC
                                                                                                                                                                                                                                                                                                                                                        WHGPHPTVKDIELSLAPEDVPV----QCNVQLDEEDYTNVEEPAQQA-----YRVVTLC
                                                                                                                                                                                                                                                                                                                                                                              WHGDTPTLHEYMLDLOPETTDLYXYXQLINDSSEEED--BIDGPAGQAEPDRAHYNIVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry version 28.
                                                                                                                                                                                                sequence version entry version 31.
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A
                                                                                                                                                                                                                                                STANDARD;
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           Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
86
9625 MW;
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                                                                                                                                                   type (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [GENOMIC DNA].
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o RNA
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/FTId=PRO_0000133426.

C-XX-C motif-1.

C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 186; DB 1;
Pred. No. 9.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4A3692CED16BCD60 CRC64;
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                                                                                                                                                    stage;
                                                                                 Cole
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                                                                    le S.T., Streeck R.E.
sequences, conserved
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                                                                                                                                                    Papillomaviridae;
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                                   and
            E7
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                                                                                                                                                                                                                                                                                                                                                                                                      Indels
           protein family.
                                   trans-activating
                                                                    genome
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RESULT 88
VE7_HPV66
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Query Match
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Q80956;
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Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN 1 93
                                                                     MOTIF
                                                                                                                              EMBL; U31794; AAA79500.1; -; Genomic_DNA.

PIR; B44890; B44890.
InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; DNA-binding; Early protein; Oncogene; Transcription; Transcription regulation.

CHAIN

Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: E7 protein has both transforming and trans-activating activaties.
-- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus tyn
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=37119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998, integrated into UniProtKB/Swiss-Prot. 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 30.
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                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/t.
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma of the uterine cervix. J. Clin. Microbiol. 29:2656-2660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tawheed A.R., Beaudenon S., Favre M., Orth "Characterization of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1663515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=E7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M73236; AAA47042.1; ALT_INIT; Genomic_DNA. PIR; F39451; W7WL42.
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                                                                                                                                                                                                                                                                                           EMBL; M75123; -; NOT ANNOTATED CDS; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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86
AA;
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89
10679 MW;
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                                             11912 MW;
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  35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA
                                                                /FTId=PRO_0000133459.
C-XX-C motif-1.
C-XX-C motif-2.
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Pred. No. 2.1e-13
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C-XX-C motif-1.
C-XX-C motif-2.
  Score 183.5;
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                                             C09339F42F62AFFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papillomaviridae,
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Attribution-NoDerivs License
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DB 1;
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Length 105;
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VEZ-HPV
ID -WE
AC Q8
DT 15
DT 01
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DT 01
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GN Na
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CC ---
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037386 CCPV1
037386;
01-JAN-1998,
01-JAN-1998,
07-FEB-2006,
  Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: E7 protein has both transforming and transactivities.
                                                                                                                                                                             Viruses; dsDNA viruses, Alphapapillomavirus.
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Scinicariello F., Soza I., Brasky K.M., Hilliard J.K.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Common chimpanzee papillomavirus type 1. Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae; primate papillomaviruses;
                                                                                                                                                                                                                                                           Protein E7
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Common chimpanzee NCBI_TaxID=66261;
                                                                             Delius H
                                                                                                                                                   NCBI_TaxID=333766;
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                                                                                                     NUCLEOTIDE SEQUENCE
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity;
GO:0006355; F:regulation of transcription, DN
erPro; IPR000148; Papvi_E7.
m; PF00527; E7; 1.
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sequence version 1.
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Pred. No. 5e-13;
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37 HPV70
57 WE7 HPV70
57 P50785;
67 01-OCT-1996, 4
67 07-FEB-2006, 6
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                                                                                                                                                                                                                                                                                                        "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70, related to the potentially oncogenic HPV39.";
J. Clin. Microbiol. 34:738-744(1996).
-!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=97060129; PubMed=8904450;
Longuet M., Beaudenon S., Orth G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=96249586; PubMed=8815087;
Forslund O., Hansson B.G.;
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InterPro; IPR000148; Papvi_E7
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                                                                                                                                                               EMBL; U21941; AAC54851.1; -; Genomic_DNA.
EMBL; U22461; AAC54881.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forslund O., Hansson B.G.;
"Human papillomavirus type 70 genome cloned from overlapping PCR "Human papillomavirus type 70 genome cloned from overlapping PCR "Thurston products: complete nucleotide sequence and genomic organization.";
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DNA-binding; Early pro
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                                                                                                         DNA-binding; Early protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCCKCDSTLRLCVQSTHVDIRTLEDLL-MGTLGIVXPICSQK 97
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                                                                                                                                              IPR000148; Papvi_E7
101
109
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sequence version 1.
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                                                                                         regulation.
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104
12657
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10565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.7%;
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o RNA stage; Papillomaviridae;
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                Protein E7.
/FTId=PRO_0000133462.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                             Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 179.5; DB 1
Pred. No. 6.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6A543269F2561891 CRC64;
       2FD3C643DFAFF891 CRC64;
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RESULT 92
VE7 HP7 H
AC P22T6
DT 01-AU
DT 07-FE
DB Name=
OS Human
OC VIVA
DS VIVA
RN NICLE
RN NICLE
RN NICLE
RN NICLE
RY MEDLI
RP NICLE
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DT 01
DT 07
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Best Local S
Matches 42
2SULT 93
37_HPV56
5 P36833;
6 01-JUN-1994,
7 01-JUN-1994,
7 07-PEB-2006,
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Best Local Similarity
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01-AUG-1991,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=91188699; Pubmed=1964523; DOI=10.1016/0168-1702(90)90091-0;
Hirsch-Behnam A., Delius H., de Villiers E.M.;
"A comparative sequence analysis of two human papillomavirus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VE7_HPV57
P22160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virus Res. 18:81-98(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation.
CHAIN 1 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
DNA-binding; Early protein; On
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          types 2a and 57."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; X55965; CAA39431.1; -; Genomic_DNA. S15622; S15622.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                              CCKCHSTVRLVVECGAADIRHLEQLFLNTLTIVCPRC 91
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                                                                                                                                                                                                                                                     CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC
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integrated into UniProtKB/Swiss-Prot. sequence version 1. entry version 31.
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                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10376 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Oncogene; Transcription;
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97
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                                                                                                                                                                                                                                                                                                                                                                                                    15;
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/FTId=PRO 0000133453.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.

C-XX-C motif-3.
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                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 178.5;
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                                                                                              105
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                                                                                                                                                                                                                                                                                                                                                                                                7.9e-13;
ches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trans-activating
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Best Local
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7_HPV07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VE7 HPV07
P36816;
01-JUN-1994,
01-JUN-1994,
07-FEB-2006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOTIF
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"Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and trans-act
                       EMBL; X74463; CAA52477.1; -; Genomic_DNA. PIR; S36585; S36585.
                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501, PubMed=8205838;
Delius H., Hofmann B.;
"Primer-directed sequencing of human papillomavirus
"Primer-directed sequencing of human papillomavirus
"Curr Top Microbiol Immunol 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type Tiruses; dsDNA viruses, no Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein E7.
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X74483; CAA52597.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphapapillomavirus.
NCBI_TaxID=10596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein E7.
                                                                                                                                                           activities.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=E7;
                                                                                                                                                                                                      Curr. Top. Microbiol. Immunol. 186:13-31(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
       IPR000148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry version 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           integrated into UniProtKB/Swiss-Prot
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                                                                                                                                                                Belongs to the papillomaviruses
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101
11892
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                                                                                                                                                                                                                                                                                                                                                                                                      e 7.
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/FTId=PRO 00001
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 178.5; DB 1
Pred. No. 9.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                  stage; Papillomaviridae;
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                                                                                                                                                                E7
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                                                                                                                                                                                                              trans-activating
                                                                                                                                                                protein family.
                                                                                                                                                                                                                                                         types.";
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Best Local
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Best Local Similarity
Matches 45; Conserv
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7_ HPV51
VE7_ HPV51
P26558;
01-AUG-1992, :
01-AUG-1992, :
07-FEB-2006, :
                                                                                                                                                                                                                                                               MOTIF
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91303675; PubMed=1649326;
Lungu O., Crum C.P., Silverstein S.J.;
Biologic properties and nucleotide sequence
papillomavirus type 51.";
J. Virol. 65:4216-4225(1991).
-!- FUNCTION: E7 protein has both transformin
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MOTIF
SEQUENCE
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Viruses; dsDNA viruses,
Alphapapillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000148; Papvi_E7 Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M62877; -; NOT_ANNOTATED
PIR; F40415; W7WL51.
                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Early protein; Oncogene; Transcription; Transcription regulation.

Transcription regulation.

1 101 Protein E7.
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                                                                                                                                                                                                                                                                                                          MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10595;
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60
                                         56
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                                                                                                                                                                                              Similarity
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APCCRCSSVVQLAVESSGDTLRVVQQMLMGELSLVCPCCA
                                    TECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                  MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE
                                                                                                                MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAH----YNIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXXYQLNDSSEEEDEIDGPAGQAEPDRAH-------
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104
111 AA;
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                               AΑ;
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107
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                                                                                                                                                                                                                                                               65
98
11339
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                                                                                                                                                                                            34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type 51.
es, no RNA stage;
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                                                                                                                                                                                                                                                               MW.
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                                                                                                                                                                                                                                                        Protein E7.

/FTId=PRO 0000133447.

C-XX-C mocif-1.

C-XX-C mocif-2.

C-XX-C mocif-2.

M; 65E85C554099801A CRC64;
                                                                                                                                                                   Score 178; DB 1; Pred. No. 1e-12; 16; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 178.5;
Pred. No. 9.9
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/FTId=PRO_0000133406
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                 Length 101;
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VE7_HPV55
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InterPro; Irkver: 1.
Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Or
DNA-cription regulation.
97
                                                                                                                                                           VE7 HPV2A
P25485;
01-MAY-1992, i
01-MAY-1992, e
07-FEB-2006, e
Protein E7.
Name=E7;
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01-NOV-1996,
07-FEB-2006,
                                                  NUCLECTIDE SEQUENCE [GENOMIC DNA].

MEDLINB=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-0;

Hirsch-Behnam A., Delius H., de Villiers E.M.;

"A comparative sequence analysis of two human papillomavirus (HPV)

types 2a and 57.";
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Q80935;
                                        types 2a and
Virus Res. 1
                                                                                                                           Human papillomavirus tyj
Viruses; dsDNA viruses,
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Alphapapillomavirus.
NCBI_TaxID=37114;
         activities.
                                                                                                                NCBI_TaxID=10584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
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-!- SIMILARITY: Belongs to the papillomaviruses E7 protein
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                              us Res. 18:81-98(1990).
FUNCTION: E7 protein has
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                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                GTCNRNVRLVVQCTGTDICQLHTLLLGSLEILCPVCAPK 96
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90
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                             protein
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o RNA stage; Papillomaviridae;
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Pred. No. 1.5e
14; Mismatches
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C-XX-C motif-2.
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       papillomaviruses
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smatches 36;
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MOTIF
SEQUENCE
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Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;
"Molecular cloning and nucleotide sequence analysis of a novel human
papillomavirus (type 82) associated with vaginal intraepithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, Alphapapillomavirus.
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091R58;
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PIR; S15615; S15615.
InterPro; IPR000148; Papvi_B7.
Pfam; PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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GG:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity
GO:0006355; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                         Pro; IPR000148; Papvi_E7.
PF00527; E7; 1.
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                                            TECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
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40.0%; Pred. No. 2e-12;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ខ្ល
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 175.5; DB 1; Pred. No. 1.8e-12;
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C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                               DB 2; Length 100;
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Best Local S
Matches 41
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01-JUN-1994,
01-JUN-1994,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                             MEDILINE=94265501; PubMed=8205838; Delius H., Hofmann B.;
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Q2VJB9;
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SEQUENCE 96 AA; 10594 MW; E791B4A9BA4B885F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 102.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
DNA-binding; Early protein; Oncogene; Transcription; Transcription regulation.

CHAIN 1 86 Protein E7.
                                                                      PIR; S36533; S36533.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                           "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and trans-act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE. STRAIN=Qv34077;
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                                                                                                                                                                                                       Copyrighted
Distributed
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Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 79:15503-15510(2005).
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10-JAN-2006,
                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the papillomaviruses E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _99API
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                                                                                                                                                   X74465; CAA52490.1; -; Genomic_DNA.
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    RNA stage; Papillomaviridae;

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Pred. No. 2.5e-12;
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and 1s
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Gapop 10.0
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Match
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1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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1 MHGDTPTLHEYMLDLQI
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9-80-523A-12

9-613-303-12

0-267-311-12

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0-267-311-3

9-485-885-1

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9-485-815-20

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US-10-267-311-19
US-09-485-885-14
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-485-885-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Applic Patent No. 5736318
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                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: GB S
PRIOR FILING DATE: 197-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
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CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                   CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner,
STREET: 200 State Street
                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 99.2%;
Local Similarity 96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
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McDaniels, Patricia A.
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Cabezon Silva, Teresa
                                                                                                                                                                                                                                                      USA
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Pred. No. 1.8e-59;
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                                                                                                                                                                                                                                                                                                                                        Ph.D.,
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US-08-075-541D-42
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                                                TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/08075541D Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.0%;
Best Local Similarity 96.9%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: ALAN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-330-1311 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
APPLICATION DATE: 10-JUN-1993
                                                                                                                                                                              NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                 STRANDEDNESS:
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                   linear
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Pred. No. 8e-60;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                            Patent No. 6228368
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08944368A Patent No. 6228368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09382616A Patent No. 6200746
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APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
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TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
                                                                                                                                      STREET: STREET: Chicago
CITY: Chicago
Thre: Illinois
Thre: Thrited
                                                                                                                                                                                                                                                                                         APPLICANT: Gissman, TITLE OF INVENTION: TITLE OF INVENTION:
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                     COUNTRY: United States of America ZIP: 60606-6402
MPUTER READABLE FORM:
 APPLICATION NUMBER:
                                                                                                                                                                                                                                    ADDRESSEE:
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96.9%;
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                                                                                                                                                                                                                                                                                         Papilloma Virus Capsomere Vaccine Formulations and Methods of Use
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US/08/944,368A
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Pred. No. 8e-60;
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Pred. No. 8e-60;
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; MOLECULE TYPE: protein US-08-944-368A-4
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Best Local Similarity
Matches 95; Conserv
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                                                                                                 TELEFAX: (202) 672-5
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: Williams Jr., Joseph.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,764

FILING DATE: 30-Mar-2001

CLASSIFICATION: CUnknown>
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TYPE: amino acid
TOPOLOGY: linear
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APPLICATION NUMBER: US 09/026,896

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102
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HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
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ADDRESSEE: FOLEY & LARDNER
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                                                             TYPE: amino acid
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                                                                              ENGTH: 98 amino acids
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Pred. No. 8e-60;
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Matches
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                                                                                                                                          Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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FILING DATE: 07-No. 6562351-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 672-5300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
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HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Pred. No. 8e-60;
0; Mismatches
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US-09-722
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US-09-824-017-4
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        STATE: D.C.
STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: SANDATION:
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 31,298
REGISTRATION INFORMATION:
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SECURENCE CHARACTERISTICS:
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APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
FILE REFERENCE: 18341/6216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09824017
Patent No. 6649167
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
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LENGTH: 98
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Best Local :
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CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
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SOFTWARE: PatentIn Ve
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ORGANISM: Papillomavirus sylvilagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
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Pred. No. 8e-60;
0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Thorgeirsson, Snorri S.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

TITLE OF INVENTION: CDNA ENCODING A GENE BOG (B5)

TITLE OF INVENTION: PRODUCT

FILE REFERENCE: 11613.29USW1

CURRENT APPLICATION NUMBER: US/09/637,746

CURRENT FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: CF(7/US99/04142)

PRIOR APPLICATION NUMBER: US 60/079,567

PRIOR APPLICATION NUMBER: US 60/079,567

PRIOR APPLICATION NUMBER: US 60/075,922

PRIOR APPLICATION NUMBER: US 60/075,922

PRIOR FILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN VETSION 3.1
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US-09-637-746-3
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LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus
S-09-637-746-3
                                                              GENERAL INFORMATION:
APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
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Best Local :
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NUMBER OF SEQ ID NOS: 25
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7
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Local Similarity 96.9%;
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Pred. No. 8e-60;
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GENERAL INCORMATION:
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURCAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
ITITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
ITITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
ITITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
ITITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
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ITITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION
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; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-7
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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US-09-613-303-12
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                                                                                                                                                                                                                                                                                Sequence 12, Application US/09613303 Patent No. 6495347 GENERAL INFORMATION:
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Pred. No. 8e-60;
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Pred. No. 8e-60;
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GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTIO
FILE REFERENCE: 12071/002001
                                                                                                                                                          RESULT 15
US-09-613-303-35
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; OTHER INFORMATION:
US-10-267-311-12
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US-10-267-311-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 12
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SOFTWARE: FastSEQ for
SEQ ID NO 12
LENGTH: 121
                                                                                                                         Sequence 35, Application US/09613303 Patent No. 6495347
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Best Local
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Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US/10/267,313
CURRENT APPLICATION NUMBER: US/09/613,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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                    12071/002001
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                                 INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
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Windows Version
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Pred. No. 1.1e-59;
0; Mismatches 3
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Pred. No. 1.1e-59;
0; Mismatches 3
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CURRENT FILING DATE: 2000-07-10;
PRIOR APPLICATION NUMBER: US 60/1:
PRIOR FILING DATE: 1999-07-08;
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Ver: SEQ ID NO 35;
SEQ ID NO 35;
LENCTH: 198
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-485-885-1
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
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; OTHER INFORMATION: fusion sequence
US-09-613-303-35
      GENERAL INFORMATION:
APPLICANT: Bruck, C
APPLICANT: Cabezon
APPLICANT: Delisse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 35
LENGTH: 198
                                                                                  Sequence 1, Application US/09485885 Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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Bruck, Claudine
Cabezon Silva, Teresa
Delisse, Anne-Marie E
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milarity 96.9%;
Conservative (
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Pred. No. 2.1e-59;
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Eva Fernande

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-1
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RESULT 19
US-08-459-818-20
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 12
LENGTH: 239
TYPE: PRT
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Sequence 12, App...
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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-09-485-885-12
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PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                    133 MHGDTPTLHEYMLDLÓPETTDLYCYEQLNDSSEEEDEIDGPAGÓAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
NT: Bruck, Claudine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                  1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                            h 99.0%;
Similarity 96.9%;
95; Conservative
                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
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                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 230
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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Pred. No. 2.4e-59;
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Sequence 20,

Application US/08459818

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Patent No. 588557
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Best Local Similarity
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 0.-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                        APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant & Gould
ADDRESSE: Merchant & Blvd., Suite 400
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APPLICANT:
APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 253 amino acids
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TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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CITY: Los Angeles
STATE: California
                                                    CITY: Los Angeles
STATE: California
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                                 COUNTRY:
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Damle, Nitin K.
Brady, William
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                                   USA
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Pred. No. 2.9e-59;
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Patent No. 5885...
Patent No. 5885...
Pringle
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REPERENCE/DOCKET NUMBER: 30436-35U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTILA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                   SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078 FILING DATE: 05-JUN-1995
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: linear
MOLECULE TYPE: protein
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CITY: Los Angeles
STATE: California
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10, 5885796
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95; Conserv
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11150 Santa Monica Blvd.,
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RESULT 22
US-08-725-776-20
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Matches
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INFORMATION FOR SEO ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                           TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
TELEFAX: 310-45-9031
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
                                                                                                                                                                                          PRIOR APPLICATION UMBER: US 08/375390
APPLICATION NUMBER: US 08/375390
FILLING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adtiano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
                                                                                             SEQUENCE CHARACTERISTICS
TOPOLOGY: 1:
                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
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nes 95; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 11150 Santa Monica Blvd., Suite 400 CITY: Los Angeles
                                   STRANDEDNESS
                                                                                                                                                       TELEPHONE: 310-445-1140
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                                                                        LENGTH:
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                                                   1: 253 amino acids amino acid
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nilarity 96.9%;
Conservative (
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-062-20
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                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/488,062 FILING DATE: 07-7UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CTLA4 Receptor TUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Adriano, Sarah REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd.,
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                      LENGTH:
                                                              216 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
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                   61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                  similarity 96.9%;
                                                                                                                                                                                                                                                                        amino acid
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 253
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                                                                                                                                                                                                                                                                                        253 amino acids
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Damle, Nitin K.
Brady, William
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sarah B
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                                                                                                                                                                                                                                                                                                                                                                                            34,470
ER: 30436-35US01
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                                                                                                                                  0; Mismatches
                                                                                                                                                Score 512; DB 1;
Pred. No. 2.9e-59;
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US-08-117-083-9
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                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
                                                                                                                                                                         Best
                                                                                                                                                       Matches
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                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       FEATURE: Protein
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
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                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                       Local
                                                                                                                                                                                                                                               LOCATION: 1..263
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                         162 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                   61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                               1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSBEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                         Similarity
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 259
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Inglis, Stephen C.
Munro, Alan J.
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                                                                                                                                                     Conservative
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                                                                                                                                                                     99.0%;
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Pred. No. 3.1e-59;
0; Mismatches 3
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                                                                                                                                                                                       Length
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; Sequence 10, Application US/08860165
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian

RESULT 25 US-08-860-165-10

Application US/08860165A

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GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: EBBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
ITILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0146
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
INUMBER: OF SEQ ID NOS: 27
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US-09-359-382-10
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LENGTH: 260
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                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human papillomavirus type
-09-359-382-10
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CURRENT APPLICATION NUMBER: US/08/860,165A

CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1995-12-20

EARLIER APPLICATION NUMBER: AU PN0157

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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                                                                                                                                    161
221 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 220
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                                                                                                                                                                                                                                                                                95;
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                                                                                                                                                                                                                                                                                                              Similarity
                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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llarity 96.9%;
Conservative
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Pred. No. 3.2e-59;
0; Mismatches 3
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Pred. No. 3.2e-59;
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RESULT 27 US-09-367-309A-1

Sequence 33, Application US/09613303 Patent No. 6495347 GENERAL INFORMATION:

APPLICANT:

Siegel, Marvin Chu, N. Randall

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CURRENT APPLICATION NUMBER: US/09/501,097A; CURRENT FILING DATE: 2000-02-09; NUMBER OF SEQ ID NOS: 25; SOETWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 25; LENGTH: 287; TYPE: PRT; ORGANISM: Human papillomavirus/Mouse US-09-501-097A-25
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US-09-501-097A-25
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CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
US-09-613-303-33
                 RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09501097A
Patent No. 6734173
GENERAL INFORMATION:
APPLICANT: TZyy-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA
FILE REFERENCE: 2240-169349
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APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING INMUNOSTIMULATING COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 266
                                                                                                                                                                                                                         Y Match 99.0%;
Local Similarity 96.9%;
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                                                                    250 CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEBDEIDGPAGQAEPDRAHYNIVTFCCK
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Pred. No. 3.2e-59;
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CURRENT APPLICATION OF A THI-LIK CURRENT APPLICATION UMBER: US/09/613,303; CURRENT FILING DATE: 2000-07-10; PRIOR APPLICATION NUMBER: US 60/143,757; PRIOR FILING DATE: 1999-07-08; NUMBER OF SEQ ID NOS: 55; SOFTWARE: FastSEQ for Windows Version 4 7; SEQ ID NO 33; LENGTH: 77-
RESULT 31
US-09-613-303-25
; Sequence 25, Application US/09613303
; Patent No. 6495347
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CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR PILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 33
LENGTH: 295
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Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mizzen, Lee A. TITLE OF INVENTION: INDUC
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                        198 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEBDEIDGPAGQABPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                                                                       61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 295
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Pred. No. 3.6e-59;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                   Length 295;
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN
FILE REFERENCE: 12071/00201
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
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US-10-267-311-25
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 324
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SEQ ID NO 25
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                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                   Query Match
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APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Local Similarity 96.9%;
287
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                                   61 CDSTLRLCVQSTHVDIRTLEDILMGTLGIVXPICSQKP 98
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                                                                                                1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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CDSTLRLCVQSTHVDIRTLEDI
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                                                                                                                                                  Conservative
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                                                                                                                                              Score 512; DB 2;
Pred. No. 4.1e-59;
0; Mismatches 3
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Pred. No. 4.1e-59;
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                                                                                                                                                                                   Length 324;
324
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US-09-485-885-14
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                                                                                                                                                                                 ; ORGANISM: Homo sapien US-09-485-885-14
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SEQ II NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14,
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APPLICANT:
APPLICANT:
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                                                                                                            Matches
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR PPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                        LENGTH: 390
TYPE: PRT
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Local Similarity 96.9%;
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o. 6342224
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                                                                        1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                             FastSEQ for Windows Version 3.0
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
VENTION: Vaccine
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                                                            Conservative
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                                                                                                                            99.0%;
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                                                                                                                            Score 512; DB 2; Length 390; Pred. No. 5.4e-59;
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                                                            OTHER INFORMATION: fusion sequence US-10-267-311-19
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US-10-267-311-19
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; SEQ ID NO 19
; LENGTH: 493
                                                                                                                                                          NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                           Patent No. 665/0-
Patent INFORMATION:
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Best Local :
Matches
                            Query Match
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               Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
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                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: fusion sequence
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ORGANISM: Artificial Sequence
                                                                                                                             TYPE: PRT
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                                                                                                                                            LENGTH:
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Score 512; DB 2; 1 Pred. No. 7.4e-59; 0; Mismatches 3;
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                            Length 493
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1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

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; Sequence 17, Application US/10267311
; Patent NO. 6657055
; GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RES
FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
pRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR APPLICATION NUMBER: US 60/143,757
pRIOR FILING DATE: 1999-07-08
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SOFTWARE: FASTSEQ for Windows V
SEQ ID NO 17
LENGTH: 639
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-613-303-17
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                                                                                  ; OTHER INFORMATION: fusion sequence US-10-267-311-17
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Query Match 99.0%;
Best Local Similarity 96.9%;
Matches 95; Conservative
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT FILINGIONIUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR PILING DATE: 1999-07-08
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 55
                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                    LENGTH: 639
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Score 512; DB 2;
Pred. No. 1.1e-58;
0; Mismatches 3
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                                      Length 639;
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FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 641
                                                                                                                                                       APPLICANT: Siegel, Marvin
APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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US-10-267-311-51
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US-09-613-303-51
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                                                                          NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 641
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Patent No. 6657055
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Patent No. 6495347
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APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
OTHER INFORMATION: fusion sequence
                 ORGANISM: Artificial Sequence FEATURE:
                                                             TYPE: PRT
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95; Conserv
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Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                   RESPONSE
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
                                CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FRABESEQ for Windows Version 4.0
SEQ ID NO 53
SEQ ID NO 53
LENGTH: 647
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US-09-613-303-53
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/10267311 Patent No. 6657055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application Patent No. 6495347
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Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
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ilarity 96.9%;
Conservative
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Pred. No. 1.1e-58;
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Pred. No. 1.1e-58
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CURRENT APPLICATION NUMBER: US/09/566,420
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 19
SOPTWARE: Patentin Ver. 2.0
LENGTH: 98
CURRENT APPLICATION NUMBER: US/10/201,764
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/99/566,420
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 19
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US-10-201-764-19
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TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-09-566-420-19
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                                                                                                                                                                                                                                                Sequence 19, Application US/10201764
Patent No. 6716623
GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CHEN, S.
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Matches 95; Conserv
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Best Local S
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Patent No. 6500641
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 95.9
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Pred. No. 3.7e-59;
1; Mismatches 3
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Pred. No. 1.1e-58;
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Sequence 8, Application US/10267311

Patent NO. 6657055

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RES

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT TILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR PILING DATE: 1999-07-08
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
APPLICANT: Mizzen, Lee A.
TITLE OF INVEXTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: fusion sequence
US-09-613-303-8
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; ORGANISM: Human papillomavirus type
US-10-201-764-19
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US-09-613-303-8
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Best Local S
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Patent No. 6495347
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.38;
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Pred. No. 1.2e-58;
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Pred. No. 3.7e-59;
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GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE-

FILE REFERENCE: 12071/002001

CURRENT APPLICATION UNMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-9

PRIOR APPLICATION NUMBER: US/9/613,303

PRIOR APPLICATION NUMBER: US/0613,303

PRIOR APPLICATION NUMBER: US/0613,757

PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 12071/002001

CURRENT FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 648
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Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Pred. No. 1.2e-58;
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Pred. No. 1.7e-57;
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Sequence 41, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: PSECIFICATION NUMBER: US/09/613,303
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US-09-613-303-41
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SEQ ID NO 41
LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                       Sequence 41, Application US/10267311 Patent No. 6657055
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Best Local
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 648
                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
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95.9%;
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95.9%;
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Pred. No. 1.7e-57;
0; Mismatches 4
                                                                            RESPONSE IN VITRO
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US-09-613-303-45
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                                                                                   Sequence 45, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 45
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SEQ ID NO 41
LENGTH: 711
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Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDICTION OF A TH1-LIKE
TITLE OF REFERENCE: 12071/002001

TYPE REFERENCE: 12071/002001

TYPE REFERENCE: 12071/002001
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Best Local
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                               Score 503; DB 2;
Pred. No. 1.9e-57;
0; Mismatches 4
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Pred. No. 1.9e-57;
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                       TH1-LIKE RESPONSE
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Sequence 20, Application US/09501097A
PATENT NO. 6734173
GENERAL INFORMATION:
APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FASE(SEQ FOR Windows Version 4.0
SEQ ID NO 45
LENGTH: 724
TYPE: PRT
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US-09-501-097A-20
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US-09-501-097A-22
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US-09-501-097A-22
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FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-45
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Best Local 9
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CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOPTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tzyy-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
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CURRENT FILING DATE: 2002-10-09
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Local Similarity 96.9%;
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; TYPE: PRT
; ORGANISM: human papillomavirus/Mycobacterium tuberculosis
US-09-501-097A-20
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Sequence 12, Application US/08860165A
PATENT NO. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
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SOFTWARE: Patentin Ve
SEQ ID NO 2
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Best Local (
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SEQ ID NO 20
LENGTH: 723
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CURRENT APPLICATION NUMBER: US/09/462,993
CURRENT FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
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APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Derivated from human papillomavirus, st OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies OTHER INFORMATION: glycoprotein, clone E7*TWR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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Pred. No. 6e-55;
0; Mismatches
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Pred. No. 4.8e-57;
0; Mismatches 3
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RESULT 58
US-08-860-165-14
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CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER: OF SEQ ID NOS: 27
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US-09-359-382-12
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LENGTH: 172
TYPE: PRT
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Matches
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
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EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
Sequence 14, Application Patent No. 6004557
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Patent No. 63063
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Best Local Similarity
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CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                     CDSTLR 66
                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09359382
                                                                                                                                                                                                                                                                 68.3%;
llarity 97.0%;
Conservative
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                   US/08860165A
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; Pred. No. 1.8e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 172;
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GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
ITILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1727/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1995-12-20
IUMBER OF SEG ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                       Best Loc
Matches
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 14
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Appli
Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                           ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description
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94 CSQKP 98
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                                                  EEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPI
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                                                                                                                     66.7%;
llarity 98.5%;
Conservative
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                                                                                                                     Score 345; DB 2
Pred. No. 2e-37;
0; Mismatches
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Pred. No 2e-37;
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                                                                                                                                                        DB 2;
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US-08-606-288-10
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US-08-606-288-7
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Sequence 10, Application US/08606288 Patent No. 5955087 GENERAL INFORMATION:
APPLICANT: Whittle, N.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,288
FILING DATE: 23-FEB-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9503786.7
FILING DATE: 24-FEB-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/00034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/00034
FILING DATE: 08-JUN-1995
PRIOR APPLICATION NUMBER: US 60/00034
APPLICATION NUMBER: US 60/00034
APPLICATION NUMBER: US 60/00034
APPLICATION NUMBER: US 60/00034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 398-324
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPOS/MS-DOS
SOFTMARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITILE OF INVENTION: Polypeptides Useful as Immunotherapeutic
ITILE OF INVENTION: Agents, and Methods of Polypeptide Preparation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Suite 3400, Four Embarcadero Center CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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5, 5955087
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Pred. No. 1e-23;
4; Mismatches 28; Indels
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Best Local Similarity
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                                                                                                                                                                                          Sequence 7, Application US/09347483 Patent No. 6123948
                                                                                                                                                                                                                                  -09-347-483-7
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Whittl
APPLICANT: Carmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acid
APPLICANT: Thompson, H.S.G.
APPLICANT: Wilson, M.J.
APPLICANT: Wilson, M.J.
TITLE OF INVENTION: Polypeptides Useful as Immunotherapeutic
TITLE OF INVENTION: Agents, and Methods of Polypeptide Prepar
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/606,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Walter H. Dreger
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                                                                                                                                                                                                                                                                                                                                   59 CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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amino acid
XGY: linear
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                                                                                                                                        Whittle, N.R. Carmichael, J.P.
                                                                                                                       Connor, S.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%; Score 247; DB 1 53.5%; Pred. No. 1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-347-483-7
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FILING DATE: 08-UN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515478.7

FILING DATE: 28-UL-1995

ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24.190
REFERENCE/DOCKET NUMBER: A-63284/F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                   TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Agents, and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                              STATE: C:
                                                                                               ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 3400,
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                          0, Application US/09347483
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                                                                                California
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Suite 3400,
                                                                                                                                                                                                                                      Thompson, H.S.G. Wilson, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                  Connor, S.E.
                                                                                                                                                                                                                                                                                                    Carmichael, J.P.
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10, Four Embarcadero Center
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                                                                                                                                                                                                   Immunotherapeutic Polypeptide Preparation
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Patent No. 6365160
GENERAL INFORMATION:
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Best Local Similarity
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RILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 951547
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: WALLET H. Dreger
REGISTRATION UMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 398-324
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WEBB, Elizabeth Ann
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amino acid

OGY: linear
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                                                                                                    COUNTRY: U.S.A. ZIP: 20007-5109
                                                                                                                                        STATE: D.C.
                                                                                                                                                   CITY: Washington
                                                                                                                                                                           STREET:
                                                                                                                                                                       ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09000094
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                                                                                                                                                                                                                                                                                                                MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
                                                                                                                                                                                                                                                                                                                                                                 MARGETTS, Mary Brigid COX, John Cooper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-63284/WHD
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                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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RESULT 65
US-10-011-749-46
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Patent No. 6726912
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                        COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,749

FILING DATE: 11-Dec-2001

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
CORRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/000,094

FILING DATE: 21-Apr-1998

APPLICATION NUMBER: WO PCT/AU96/00473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 839 MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 896
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                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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FILING DATE: 21-Apr-1998
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10011749
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        John Cooper
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Best Local Similarity
Matches 52; Conserve
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US-09-000-094-22
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                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: Unknown>
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APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  839 MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHGDTPTLHEYMLDLQ-PETTDLYXXXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
                                                                                 APPLICATION NUMBER: WO PCT/AU96/00473 FILING DATE: 26-JUL-1996 APPLICATION NUMBER: AU PN 4439/95 FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1587 amino acids
TYPE: amino acid
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TELEFAX: (202) 672-5399
                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 7
REFERENCE/DOCKET NUMBER: 017227/0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09000094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%; Score 243; DB 2; llarity 52.5%; Pred. No. 1.3e-22; Conservative 15; Mismatches 28
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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ETTS, Mary Brigid
John Cooper
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RESULT 67
US-10-011-749-22
Sequence 22, Application US/10011749
Patent No. 6726912
GENERAL INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-000-094-22
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INFORMATION FOR SEQ ID NO: 22:
                                     INFORMATION
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 27-UL-1996
APPLICATION NUMBER: WO PCT/AU96/DATA
APPLICATION NUMBER: WO PCT/AU96/DATA
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Local Similarity 51.5%;
les 51; Conservative 1
                                                                                                                                                  NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: FOLEY & LARDNER
SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
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TYPE: amino acid
                                                                                                            TELEPHONE:
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MARGETTS, Mary Brigid
COX, John Cooper
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                                                                      (202) 672-5300
202) 672-5399
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(02) 672-5399
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RESULT 68
US-09-000-094-24
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US-09-000-094-24
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Patent No. 6365160
GENERAL INFORMATION:
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                                                                                                                      INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE; Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION EXPRESSION - UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
TILING DATE: 26-JUL-1996
TILING DATE: 26-JUL-1996
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                                                                                                                                                                                                                          APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-7UL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
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                                                                                                LENGTH: 465 amino acids
                                                                                                                                                                TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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Pred. No. 4.5e-23;
6; Mismatches 28
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; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-011-749-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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US-10-011-749-24
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Best Local (
                                                              Query Match
Best Local Similarity
                                          Matches
                                                                                                                                                                                                                                                                             TELEPHONE: (202) 672-51
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/011,749
PILING DATE: 11-Dec-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDWARDS, Stirling John TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WEBB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 248
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                                          51;
1 MHGDTPTLHEYMLDLQ-PETTDLYXXXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 46.4%;
Similarity 51.5%;
51; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C
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                                        46.4%; Score 240; DB 2; Length 465; ilarity 51.5%; Pred. No. 6.1e-23; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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                                                                                                                                                                                                                                                                                                                          (202) 672-5300
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                                     Gaps
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US-09-501-097A-6
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; ORGANISM: Homo sapien
US-09-485-885-19
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US-09-485-885-19
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Patent No. 6342224
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 38
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APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09501097A Patent No. 6734173
                                                                                                                                                        Matches
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SEQ ID NO 19
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 40.4%; Score 209; DB 2; Local Similarity 100.0%; Pred. No. 2.4e-20; nes 38; Conservative 0; Mismatches 0;
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 LHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 209
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172 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 217
                                                                         114 MHGPKATLQDIVLHLEPQNEIPVDLLGHQQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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                                  52 YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                               1 MHGDTPTLHEYMLDLQPET----TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                        42;
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                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
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                                                                                                                                                        Conservative
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                                                                                                                                                    39.0%; Score 201.5; DB: 39.6%; Pred. No. 2.8e-18; ative 20; Mismatches 33
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Sequence 23, App.
; Sequence 23, App.
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Ghislaine
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US-08-117-083-13
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Matches
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Patent No. 5719054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compo
OPERATING SYSTEM: PC:-
SOFTWARE: Patentin Rei
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APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Malter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESSE: Walter H. Dreger
ADDRESSE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein LOCATION: 1..272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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STATE: CA
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                                                                                                                                                                                                                                                                                                              222 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ 267
                                                                                                                                                                                                                                                                                                                                                                                           164 MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                     52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.8%; Score 200.5; DB 1; 39.6%; Pred. No. 4.8e-18; 70. Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Xaa refers to stop codon in the open reading frame."
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FILE BOTALLING STATES OF THE STEERENCE: B45107
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
SEQ ID NO 16
LENGTH: 227
                                  RESULT 75
US-08-934-915-52
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PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows V
Sequence 52, Application US/08934915 Patent No. 5932412
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LENGTH: 383
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09485885 Patent No. 6342224
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lombardo-Bencheikh, Angela TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                               52 YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                       1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                            HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ
                                                                                                                                                                                    MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDEVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-02-18
IBER: PCT/EP98/05285
                                                                                                                                                                                                                                                                               37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB 9717953.5
                                                                                                                                                                                                                                                             20;
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Pred. No. 7.7e-18;
                                                                                                                                                                                                                                                                               Score 192.5; DB : Pred. No. 4.3e-17
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                Length 227;
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                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                             Gaps
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GENERAL INFORMATION:

APPLICANT:

CHENG DILLNER, DILLNER, JOAKIM HWEE-MING

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SYNTHETIC PEPTIDES OF HUMAN

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; MOLECULE TYPE: peptide
US-08-934-915-52
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 76
                                                                                                                        GENERAL INFORMATION:
APPLICANT: HOPÉ1, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
PRIOR FILING DATE: 1997-08-27
                                                             NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.1%; Score 171; DB 1; Best Local Similarity 100.0%; Pred. No. 1.8e-15; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09486394 Patent No. 6478749
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

ODERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION NUMBER: US/08/934,915

PILING DATE: 22-SEP-1997

CLASSIFICATION LATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                           LENGTH: 30
DRGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 30 amino acid
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TITLE OF INVENTION:
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TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 QAEPDRAHYNIVTFCCKCDSTLRLCVQSTH 73
                                           30
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US-08-934-915-53
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                                                                                                                            Matches
                                                                                                                                                                                             Query Match
                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: Windows 3.0
SOPTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/934,9:
FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DILLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER'INFORMATION: E7 peptide.
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TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE MASON & ASSOCIATES, P.A.
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, 8
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,13:
RETERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                               30 amino acids
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DILLNER, LENA
CHENG, HWEE-MING
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                                                                                                                               Conservative
                                                                     31.3%; or 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES 193
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30
                                                                                                                                                              2.8e-1
                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                             Length 30
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                                                                                                                            Gaps
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GENERAL INFORMATION:

APPLICANT: HOPE1, Reinhard

TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

FILE REFERENCE: 032929-001

CURRENT APPLICATION NUMBER: US/09/486,394

CURRENT FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: FOT/EP98/04773

PRIOR FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: DE 197 37 409.3

PRIOR APPLICATION NUMBER: DE 197 37 409.3

PRIOR FILING DATE: 1997-08-27

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Batentin version 3.1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 79
US-08-934-915-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 30

TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Appropries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09486394
Patent No. 6478749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                      COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,13
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                 APPLICATION NUMBER: US/01 FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                            STREET: 17757 U.S
                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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Similarity 93.3%;
                                                                                                                                                                                                                                                                                                                                                                                   FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08934915
                                                                                                                                                                                                                                                                                                                                                                                                                       E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLNER, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                   US/08/934,915
                                                      37, 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 154; DB 2;
Pred. No. 3.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
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; ORGANISM: Human papillomavirus type 16; PEATURE; NAME/KEY: PEPTIDE; LOCATION: (1)...(30); OTHER INFORMATION: E7 peptide. US-09-486-394-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09486394
Patent No. 6478749
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08075541D Patent No. 6183745
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 30
TYPE: PRT
                                                                                                                                                                        APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL,
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                          ZIP: 19103-2398
                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIV 90
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                                                                            PENNSYLVANIA
                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.6%; Score 153; DB 2;
100.0%; Pred. No. 4.4e-13;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 1;
Pred. No. 4.4e-13;
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                                                                                                                                                       US-09-828-645-7
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LECTURE 12.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09828645
Patent No. 6743593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.1%;
Best Local Similarity 56.6%;
Matches 30; Conservative
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  OTHER INFORMATION: Derived from the E7 early region of HPV-16 NAME/KEY: misc feature LOCATION: (19) _ (19) OTHER INFORMATION: Xaa = L-carboxymethylcysteine
                                                                                                                                                                                                                                                              LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-JUN-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EYMLDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i: 32 amino acids amino acid
                                                                                           Similarity
                                   PTLHEYMLDLQPETTDLYXXXQLNDSSEEE 35
PTLHEYMLDLQPETTDLYXYEQLNDSSEEE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                         28.6%;
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                                                                       Score 148; DB 2
Pred. No. 2e-12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150.5; DB Pred. No. 1e-12; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GIDGPÄGQÄEPDRÄHYNIVTFCCKCD 32
                                                                                                             DB 2; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                           Indels
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                                                                         Gaps
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RESULT 83

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// MOLECULE TYPE: peptide
US-08-363-586-1
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                                                                                                                                                                                                                                                                                                                                                                       RESULT 84
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                                                                                                                                                                                                               Sequence 3, Application US/09828645
Patent No. 6743593
GENERAL INFORMATION:
APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08363586 Patent No. 5629161
                                                             NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                             CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1300 1 50
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 30 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          PTLHEYMLDLQPETTDLYCYEQLNDSSEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTLHEYMLDLQPETTDLYXXXQLNDSSEEE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.4%;
ilarity 93.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1994
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Pred. No. 2.7e-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 30;
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RESULT 86
US-09-486-394-2
; Sequence 2, Application US/09486394
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                                                                                                                                                                                                                                              ; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-934-915-54
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US-08-934-915-54
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
ENTING DATE: 107/949,836
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION UNMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8, TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56, TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA APPLICANT: CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                   69 VQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                VQSTHVDIRTLEDLLMGTLGIVCPICSQKP 30
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                                                                                                                                                                                                                                                                                                                                                                                                813-538-3820
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                      28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37,133
                                                                                                                                                                     Score 146; DB 1; Length 30; Pred. No. 3.7e-12; O; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 147; DB 2;
Pred. No. 2.7e-12;
0; Mismatches 2
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CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
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LENGTH: 30
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Best Local :
                                             APPLICATION UNMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
TELEFAX: 21
INFORMATION FOR
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human papillomavirus type FEATURE: NAME/KEY: PEPTIDE LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TINDLE, ROBE APPLICANT: FERNANDO, GE APPLICANT: FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103-2398
                                     TELEPHONE:
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6183745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1601 MARKET STREET, 36TH FLOOR
                  215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                     215-567-2020
SEQ ID
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Pred. No. 5e-12;
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                                                                                                                                                                                                                                                                                                                                                           Version #1.25
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; NAME/KEY: PEPTIDE
; LOCATION: (1)..(28)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-5
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                                                                                                                                                                                                                                                                                                                                                                       US-08-363-586-2
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                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08363586 Patent No. 5629161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
LENGTH: 28
TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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Patent No. 6478749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REPERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR PPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       APPLICANT:
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                               APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6
TITLE OF INVENTION: Peptides for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                   STREET: 1300
CITY: Washington
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                                                                                                                                 ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 STHVDIRTLEDLLMGTLGIVXPICSQKP 98
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27; Conservative
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                                                                                                                                                                                                                                 and E7-Gene Derived
Diagnostic Purpose
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US-08-363-586-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAFING SYSTEM: PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: AU pk 3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
        APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
                                                                                                           APPLICATION NUMBER: AU P
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 NDSSEEEDEIDGPAGQAEPDRAHYN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NDSSEEEDEIDGPAGQAEPDRAHYN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0, Application US/08075541D 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                  PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERNANDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TINDLE, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202-408-4000
                                                                                                                                                                                                              10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.3%; Score 136; DE 100.0%; Pred. No. 6e-ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/909,296
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8795-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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TELEPHONE:

215-567-2020

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                                                                                                 , MOLECULE TYPE: peptide US-08-934-915-71
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US-08-934-915-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
TORTICATION NUMBER: US/08/934,915
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71, Appl
Patent No. 593241
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & AS
STREET: 1757 U.S. HW
CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y Match 24.4%;
Local Similarity 96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 22-SEP-1997
                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                            TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
58 CCKCDSTLRLCVQSTHVDIRTLEDLLMGT 86
                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 THVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                     : 30 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THYDIRTLEDLLMGTLGIVCPICSQK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08934915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILLNER,
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                                                  23.6%;
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                                                                                                                                                                                                                                                                                                           37, 133
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                              Score 122; DB 1;
Pred. No. 5.5e-09;
4; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 126; DB 2;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                1946.6
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                                                                 Length 30;
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                                  Indels
                                  0,
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                              Gaps
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US-08-075-541D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-980-523A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. :
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08075541D Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09980523A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: TINDLE, ROBERT

APPLICANT: FERNANDO, GERMAIN

APPLICANT: FRAZER, IAN

TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSE: PANITCH SCHWARZE JACOBS & NADEL, P.C.

STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                            ZIP: 19103-2398

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, VG

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV. THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 A0 INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FROU/01513
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: FR 99/07012 PRIOR FILING DATE: 1999-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHOPPIN,
APPLICANT: BOURGAU
APPLICANT: GUILLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 23
TYPE: PRT
ORGANISM: Human Papillomavirus
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00
                                                                                    APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-UUN-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               CITY: PHILADELPHIA
STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GDTPTLHEYMLDLQPETTDLYXY 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDTPTLHEYMLDLQPETTDLYCY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOURGAULT VILLADA, IS GUILLET, JEAN-GERARD CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.4%;
  pct/au91/00575
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Pred. No. 5.2e-09;
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                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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FILING DATE:

12-DEC-1991

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US-08-934-915-48
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; MOLECULE TYPE: US-08-934-915-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08934915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTURNATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-
TELECOMMUNICATION INFORMATION:
TOT.EDHONE: 215-567-2020
                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER STATE: FLORIDA COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                         LENGTH: 20 amino
TYPE: amino acid
                                TOPOLOGY:
                                                                                                                                      TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 GOAEPDRAHYNIVTFCCKCD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQAEPDRAHYNIVTFCCKCD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILLNER, JOAKIM
DILLNER, LENA
CHENG, HWEE-MING
CHENG, HWEE-MING
VENTION: SYNTHETIC PEPTIDES OF HUMAN
VENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
VENTION: PAPILLOMAVIRUS 1, 33 AND 56,
VENTION: USEFUL IN IMMUNOASSAY FOR
                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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100.0%; Pred. No. 5.8e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               07/949,836
                                                                                                                                                                                                        37, 133
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APPLICANT: Nicland, John
APPLICANT: Nicland, John
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/036001
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 2000-05-31
PRIOR PILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73
LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-73
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                                                                               ; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-980-177A-73
                                                                                                                                                                                                               Sequence 74, Application US/09980177A
Patent No. 6838084
GENERAL INFORMATION:
APPLICANT: Vochmus, Ingrid
APPLICANT: Vicland, John
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/036001
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: DCT/EP00/05006
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 1999-66-01
NUMBER: FSEO TO NOC. 77
                                                                                                                                                              NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Patent No. 683808
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Best Local Similarity
                   Query Match
Best Local Similarity
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  Matches
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  Conservative
                     22.4%; Score 116; DB 2; 100.0%; Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.8%; Score 118; DB 2; 100.0%; Pred. No. 1.1e-08;
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    Mismatches
                                      Length 20;
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Indels
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RESULT 98
US-08-934-915-46
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US-08-075-541D-3
                                                                                                                           Sequence 46, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UWN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
APPLICATION NUMBER: pct/au91/00575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE.
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETI
TITLE OF INVENTION: PAPILLOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                               44 QAEPDRAHYNIVTFCCKCD 62
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                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                          1 QAEPDRAHYNIVTFCCKCD 19
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                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                      22.1%; Score 114; DB 2; ]
ilarity 100.0%; Pred. No. 3.3e-08;
Conservative 0; Mismatches 0;
SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                                             Length 19;
                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6183745
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/08075541D Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE TITLE OF INVENTION: PEPTIDES FOR USE THEREIN NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                         APPLICANT: TINDLE, ROBE APPLICANT: FERNANDO, GE APPLICANT: FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-8EP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows 3.0 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM For compatible
COMPUTER: Grant utilized 3
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 17757 U.:
CITY: CLEARWATER
STATE: FLORIDA
                   APPLICATION NUMBER:
                                                                                                                                                                                                  CITY: PHILADELPHIA
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                               TINDLE, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%; 5--
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                GERMAIN
               US/08/075,541D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37,133
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Pred. No. 4.9e-08;
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Sequence 69, Application US/09980177A

Patent No. 6838084

Patent No. 6838084

GENERAL INFORMATION:

APPLICANT: Jochnums, Ingrid

APPLICANT: Nieland, John

TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the

TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and

TITLE OF INVENTION: Therapy

FILE REFERENCE: 50125/036001

CURRENT APPLICATION NUMBER: US/09/980,177A

CURRENT PILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: PCT/EP00/05006

PRIOR APPLICATION NUMBER: DE 19925199.1

PRIOR APPLICATION NUMBER: DE 19925199.1

PRIOR PILING DATE: 2000-05-31

PRIOR PILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 77

SOFTMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 69

LENGTH: 20

ORGANISM: Human papillomavirus type 16

US-09-980-177A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-43
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US-09-980-177A-69
Search completed: May 27, 2006, 05:18:34 Job time : 30.7309 secs
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TELEPAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                             Query Match 21.7%; Score 112; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 6.6e-08; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.7%; Score 112; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 6.6e-08; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
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US-10-368-046-1
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Result No.

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Minimum Maximum

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Title: Perfect so Sequence:

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; TYPE: PRT
; ORGANISM: Homo sapien
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                                                                                                                                                                       NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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Publication No. US20020182221A1
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LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
5-10-530-253-11
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                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT PILING DATE: 2005-04-04
PRIOR FILING DATE: 2005-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-03
                                            Query Match
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva,
APPLICANT: Delisse, Anne-h
APPLICANT: Gerard, Catheri
APPLICANT: Lombardo-Benche
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Vaccine FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10530253
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                      99.2%;
  Score 513; DB 4; Length 220; Pred. No. 3.8e-53; O; Mismatches 3; Indels
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Gaps
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Sequence 9, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
    APPLICANT: Cassetti, Maria C.
    APPLICANT: Smith, Larry
    APPLICANT: Susan p. McElhiney
    TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/L00M137-US2
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR PILING DATE: 2003-10-02
; PRIOR FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; EQ ID NO 9
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GEB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius
OTHER INFORMATION: influenzae B and mutated E7 from Human papilloma
OTHER INFORMATION: virus type 16)
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 MHGDTPTLHEYMLDLÓÞETTDLYGYQÓLNDSSEEEDEIDGPAGÓAEPDRAHYNIVTFCCK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 3.8e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 220
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                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein US-10-367-095-9
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RESULT 6
US-10-368-046-9
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/356,154
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,135
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/356,113 PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
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CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line FILE REFERENCE: 44149-1US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/356,123 FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/356,156 FILING DATE: 2002-02-14
                                                                                                                                                             471 MHGDTPTLHEYMLDLQPETTDLYGYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 530
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                                                                                                    61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP 98
                                                                                                                                                                                                                                           95;
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                                                                                                                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                            Similarity
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                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 568
                                                                                                                                                                                                                                           Conservative
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Pred. No. 4.4e-53;
                                                                                                                                                                                                                                                            Score 513; DB 4; Length 805; Pred. No. 1.9e-52;
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RESULT 7
US-10-367-367-9
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CURRENT APPLICATION NUMBER: US/10/367,367
CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR TILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
                                                                                                                                                                                                                                                      Sequence 9, Application US/10367367
Publication No. US20040121465A1
GENERAL INFORMATION:
APPLICANT: Robin A. Robinson
TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Virus-Like Particles for Express:
FILE REFERENCE: 44149-2US1
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Publication No. US20040063188A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR APPLICATION NUMBER: US 60/356,156
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CURRENT FILING DATE: 2003-02-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Method for TITLE OF INVENTION: Expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/356,113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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Pred. No. 1.9e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                         Expression
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APPLICANT: NOVAVAX, INC., et al.

APPLICANT: NOVAVAX, INC., et al.

APPLICANT: NOVAVAX, INC., et al.

TITLE OF INVENTION: Optimization of Gene Sequences of

TITLE OF INVENTION: Chimeric Virus-Like Particles for Expression in Insect Cells

FILE REFERENCE: 19065/2132

CURRENT APPLICATION NUMBER: US/10/918,337

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR APPLICATION NUMBER: US 60/356,154

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

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PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-918-337-9
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                                                                                                                                                                                            Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
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     Matches
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Best Local
                             Query Match
Best Local Similarity
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                                                                                                                    FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
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        95;
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        Conservative
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Score 513; DB 5;
Pred. No. 1.9e-52
0; Mismatches
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Pred. No. 1.9e-52;
                                                        DB 5; Length 805;
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RESULT 10
US-09-820-765-4
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US-09-728-466-1
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APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
RITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09820765
publication No. US20020039584A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILICMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PRT
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/:
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                CITY: Washington
STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                   COMPUTER: IBM PC compatible
operating system: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: CUNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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96.9%;
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Pred. No. 1.8e-53;
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RESULT 11
US-09-824-017-4
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US-09-824-017-4
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Best Local Similarity 96.9%;
Matches 95; Conservative
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TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                            NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/026,896 FILING DATE: 1998-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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                                                                                                                                                                       TELEPHONE: (202) 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                          672-5399
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Pred. No. 1.8e-53;
0; Mismatches 3
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: 9 US-09-986-118A-4
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REFERENCE/DOCKST NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acide
TYPE: amino acide
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Best Local Similarity
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,118A

FILING DATE: 07-NO. US20030021806A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

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Local Similarity 96.9%;
hes 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
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                           61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 98
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                                                                                                                                                                                                                                                                                        Score 512; DB 3;
Pred. No. 1.8e-53;
0; Mismatches 3
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Pred. No. 1.8e-53;
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RESULT 13 US-10-177-390-8

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US-10-654-129-4
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APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynuclectides by Electroporation
FILE REFERENCE: 021505w0/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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INFORMATION
                                                     APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING YSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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               TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
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ZIP: 20007-5109
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Pred. No. 1.8e-53
0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Thorgeirsson, Snorri S.

APPLICANT: Woitach, Joseph T.

APPLICANT: Woitach, Joseph T.

ITILE OF INVENTION: CORA ENCODING A GENE BOG (B5T OVER-EXPRESSED GENE) AND ITS PROTEIN TITLE OF INVENTION: CURCENT BODUCT

FILE REFERENCE: 11613.29USW1

CURRENT APPLICATION NUMBER: US/10/772,988

CURRENT FILLING DATE: 2004-02-05

PRIOR APPLICATION NUMBER: US/09/637,746

PRIOR APPLICATION NUMBER: US/09/637,746

PRIOR APPLICATION NUMBER: DCT/US99/04142

PRIOR APPLICATION NUMBER: US 60/079,567

PRIOR APPLICATION NUMBER: US 60/079,567

PRIOR APPLICATION NUMBER: US 60/075,922

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-03-25

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-25
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US-10-772-988-3
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Sequence 5, Application US/10479541
Publication No. US20040151723A1
GENERAL INFORMATION:
APPLICANT: Kirin Beer Kabushiki Kaisha
TITLE OF INVENTION: Novel E7 antigen epitope from human
TITLE OF INVENTION: CD4+ T cells activated thereby
FILE REFERENCE: 137240PX
CURRENT APPLICATION NUMBER: US/10/479,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 98
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nilarity 96.9%;
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 173803/2001
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 98
LENGTH: 98
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LENGTH: 98
TYPE: PRT
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                                                                                                                                                                                             Sequence 1, Application US/10657399 Publication No. US20050032038A1 GENERAL INFORMATION:
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APPLICANT: GISSMANN, et al.

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE

FILE REPERENCE: 27013/38150

CURRENT APPLICATION NUMBER: US/10/042,526A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: US 09/632,286

PRIOR FILING DATE: 2000-06-03

PRIOR APPLICATION NUMBER: US 08/944,368

PRIOR APPLICATION NUMBER: US 08/944,368

PRIOR FILING DATE: 1997-10-06

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.3
APPLICANT: Pisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/10/657,399
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US/09/728,466
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -10-042-526A-4
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llarity 96.9%;
Conservative
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Pred. No. 1.8e-53;
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RESULT 20
US-10-343-448-5
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US-10-858-384-12
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Sequence 5, Application US/10343448

Publication No. US20050054820A1

GENERAL INFORMATION:
APPLICANT: WU, TZYY-Choou
APPLICANT: HUNG, Chien-Fu
TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
FILE REFERENCE: 2240-186463
CURRENT APPLICATION NUMBER: US/10/343,448
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. :
SEQ ID NO 12
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADD
APPLICANT: GUILLET, JEAN-GEI
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APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: PERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR TO OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
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CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
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TYPE: PRT
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ORGANISM: Papillomavirus sylvilagi
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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2003-01-31

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APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Cool, Chean Eng
TITLE OF INVENTION: Complexes and Methods of
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
VUMBER OF SEQ ID NOS: 198
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 17
LENGTH: 98
TYPE: PRT
ORGANISM: Homo Bapiens
US-10-367-057-17
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US-10-530-253-14
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US-10-367-057-17
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LENGTH: 98
TYPE: PRT
                                                        GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/10367057 Publication No. US20050100554A1 GENERAL INFORMATION:
                                                                                                                                                  Sequence 14, Application US/10530253
Publication No. US20060014926A1
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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APPLICANT: Jeffrey K. Fullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/24134
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/222,902
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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pred. No. 1.8e-53;
0; Mismatches 3;
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APPLICANT: FTAZEY, IAN HECTOY
APPLICANT: FTAZEY, IAN HECTOY
FILE OF INVENTION: Gene Expression System Based on
FILE REFERENCE: 10338-1110
CURRENT APPLICATION NUMBER: US/11/077,939
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/AU2003/001200
PRIOR FILING DATE: 2003-09-12
PRIOR FILING DATE: 2003-09-12
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 28
SOFYMARE: PATENTIN VERSION 3.2
SEQ ID NO 5
LENGTH: 98
TURN: DATE: 98
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; TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-530-253-14
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US-11-179-478-4
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US-11-077-939-5
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                                                 Sequence 4, Application US/11179478

Publication No. US20050249745A1

GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
APPLICANT: HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/11077939 Publication No. US20050196865A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
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Best Local Similarity
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PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
               CORRESPONDENCE ADDRESS:
                                   NUMBER OF SEQUENCES:
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FOLEY & LARDNER
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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STREET:

3000 K Street, N.W.

Washington D.C.

U.S.A.

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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RES
TITLE REFERENCE: 12071/002001
CURRENT FAPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
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                                    ; OTHER INFORMATION: fusion sequence US-10-267-311-12
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Best Local Similarity
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/11/179,478
FILING DATE: 13-JULY-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                     ORGANISM: Artificial Sequence
                                                                           FEATURE:
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LENGTH: 98 amino acids
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NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dolor
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TOPOLOGY: linear
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99.0%; Score 512;
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Pred. No. 1.8e-53;
0; Mismatches 3
BB
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Length 121;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
ITITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTMARE: PRACESEQ for Windows Version 4.0
SEQ ID NO 12
PRIOR FILING DATE: 1991-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-12
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                                                                                                                     APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/10267311 Publication No. US20030050469A1 GENERAL INFORMATION:
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Publication No.
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Matches 95; Conservative
                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 35
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Best Local Similarity
                                                                                                    NUMBER OF SEQ ID NOS:
                      LENGTH: 198
TYPE: PRT
ORGANISM: Artificial Sequence
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No. US20050089841A1
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0; Mismatches 3;
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Pred. No. 2.4e-53;
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                                                                                                                                                                                                                                                                                 RESPONSE IN VITRO
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
SECTION
                                                                                                                                                                                                                                                                              RESULT 29
US-10-000-903-1
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US-10-679-956-35
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Best Local S
Matches 95
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Publication No. US20020182221A1
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                                                                                                           APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Benchekh, Angela
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FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                             APPLICANT: Gerard, Catherin
APPLICANT: Lombardo-Benche
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: fusion sequence
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Similarity 96.9%;
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Pred. No. 4.4e-53;
0; Mismatches 3
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Pred. No. 4.4e-53;
0; Mismatches 3
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GENERAL

INFORMATION:

Claudine

APPLICANT: Bruck, APPLICANT: Cabezo APPLICANT: Delige

Cabezon Silva, Teresa Delisse, Anne-Marie Eva Fernande

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RESULT 31
US-10-000-903-12
Sequence 12, Application US/10000903
Publication No. US20020182221A1
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CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: ETT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR PRILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 220
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Matches
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
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TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E7 from Human papilloma virus type OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                 174
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                                                                                                                                                    61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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95; Conser
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                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
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Pred. No. 5e-53;
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Pred. No. 5e-53;
D; Mismatches
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; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus ; OTHER INFORMATION: pneumoniae and E7 from Human papilloma virus type ; OTHER INFORMATION: 16)
US-10-899-771-12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-12
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
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LENGTH: 239
TYPE: PRT
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                     Local Similarity
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  193
                              61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                         MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lombardo-Bencheikh, Angela
                                                                                                                                                                                Conservative
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                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                   Score 512; DB 5;
Pred. No. 5.5e-53;
                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                          Length 239;
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Sequence 2, Application US/11192923A

Publication No. US20060018928A1

GENERAL INFORMATION:

APPLICANT: PANG, XIAOWU

ITILE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS

TITLE OF INVENTION: RECOMBINANT REPLICON

FILE REFERENCE: 11620-003

CURRENT APPLICATION NUMBER: US/11/192,923A

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: CN 03115272.4

PRIOR APPLICATION NUMBER: CN 03115273.2

PRIOR APPLICATION NUMBER: CN 03115273.2

PRIOR FILING DATE: 2003-01-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 3.3

SEQ ID NO 2

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US-10-530-253-7
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US-11-192-923A-2
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Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                          Matches
                                                                                                                                                                                               Query Match
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APPLICANT: Susan P. McElhiney
TITLE OP INVENTION: HUWAN PARILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                      ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                               Local Similarity
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                                                                                                   1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP 98
                                                                           MIGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQABPDRAHYNIVTFCCK
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Pred. No. 5.8e-53;
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Pred. No. 6e-53;
                                                                                                                                                             Mismatches
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APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/9/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
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                                                                                                                          Matches
                                                                                                                                                            Query Match
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PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHARLATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/AU98/00080 PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 99.0%;
Local Similarity 96.9%;
                                          198
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 257
                                                                MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                        Conservative
                                                                                                                                       96.9%;
                                                                                                                     Score 512; DB 4;
Pred. No. 7.2e-53;
0; Mismatches 3
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Pred. No. 6.3e-53;
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APPLICANT: Siegel, Marvin
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION SATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                               ; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: fusion sequence US-10-679-956-33
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                                                                                                                                                                                              SEQ ID NO 25
LENGTH: 324
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
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Best Local Similarity
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    Matches
                    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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    Conservative
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                  99.0%;
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Score 512; DB 4;
Pred. No. 8.1e-53;
0; Mismatches 3
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Pred. No. 7.2e-53;
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                                        Length 324;
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US-10-472-724-10
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CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/10472724
Publication No. US20040171806A1
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LENGTH: 324
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                                                                                                SOPTWARE: PatentIn version 3.2 SEQ ID NO 10 LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                PRIOR APPLICATION NUMBER: EP 01107271.7 PRIOR FILING DATE: 2001-03-23
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 4121-154
                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                   OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK
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No. US20050089841A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 5;
Pred. No. 8.1e-53;
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                                                                                                                                                                                                                                                                                                                              proteins useful for vaccination
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Query Match
Best Local Similarity
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US-10-000-903-6
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US-10-899-771-6
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                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10899771 Publication No. US20050031638A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 6
                                                       PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR EILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                 FILE REFERENCE: 845124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
                                                                                                                                                                                                                                             APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Pa
TITLE OF INVENTION: and Fusion Proteins Adjuvanted
                                        NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: B45107
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Pred. No. 8.4e-53;
0; Mismatches 3
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Pred. No. 9.5e-53;
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juvanted with a CpG Oligonucleotide
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Sequence 14, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human
TITLE OF INVENTION: and Fusion Proteins Adjuvan
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
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US-10-899-771-14
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US-10-000-903-14
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fei
APPLICANT: Gerard, Catherine Marie Ghi
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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-10-899-771-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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No. US20020182221A1
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llarity 96.9%;
Conservative
                                                                   and Fusion Proteins Adjuvanted
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Pred. No. 1e-52;
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Pred. No. 9.5e-53;
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                                                                   Human Papilloma Virus Proteins
juvanted with a CpG Oligonucleo
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                                                                   CpG Oligonucleotide
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PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTMARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
                                                                                                                                                                                                                                      ; ORGANISM: Chimaeric US-10-296-770-7
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CURRENT APPLICATION NUMBER: US/10/296,770

CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: PCT/EPO1/06952

PRIOR APPLICATION NUMBER: GB 0015619.0

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10296770 Publication No. US20030104570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cabezon Silva, Teresa Elisa Virginia
APPLICANT: Delisse, Anne-Marie Eva Fernande
TITLE OF INVENTION: Triple Fusion Proteins Comprising
TITLE OF INVENTION: Ubiquitin Fused Between Thioredoxin and a
TITLE OF INVENTION: Interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                           LENGTH: 421
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344
375 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 412
                                                                            315 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                    61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                            Score 512; DB 4;
Pred. No. 1.1e-52;
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Pred. No. 1e-52;
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                                                                                                                                                                                              Length 421;
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RESULT 46 US-10-267-311-19

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FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR PILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PABESEQ for Windows Version 4.0

SEQ ID NO 19
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/10679956
Publication No. US20050089841A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR TILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Siegel, Marvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 493
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                       ENGTH:
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                                                              396 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                         61
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                                                                                                                                                                                                                                                                                                                           493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                              95; Conservative
                                                                                                                                                            Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                     MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                            99.0%;
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                                                                                                                                          Score 512; DB 5; L
Pred. No. 1.4e-52;
0; Mismatches 3;
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Pred. No. 1.4e-52;
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RESULT 49
US-10-679-956-17
; Sequence 17, Application US/10679956
; Publication No. US20050089841A1
; GENERAL INFORMATION:
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE:
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,757
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US/09/143,757
PRIOR FILING DATE: 1999-07-08
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APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.
TITLE OP INVENTION: INDUCTION OF A TH1-LIKE RE:
FILE REFERENCE: 12071/002001
CURRENT APPLICATION UNMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/9/613,303
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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                                                                                                                          ; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-679-956-17
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                                        Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                     LENGTH: 639
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 639
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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milarity 96.9%;
Conservative
                                          Conservative
                                                            99.0%;
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                                                            Score 512; DB 5;
Pred. No. 1.9e-52;
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Pred. No. 1.9e-52;
                                          Mismatches
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                                                                                Length 639;
                                          Indels
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                                          Gaps
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
ITILE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTMARE: PastSEQ for Windows Version 4.0
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILLING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,757
PRIOR APPLICATION NUMBER: US 60/143,757
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US-10-679-956-51
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US-10-267-311-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 51
LENGTH: 641
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Publication No.
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NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
                                                            LENGTH: 641
TYPE: PRT
OTHER INFORMATION: fusion sequence
               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542
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No. US20030050469A1
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Pred. No. 1.9e-52;
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FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 647
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 53
US-10-679-956-53
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; OTHER INFORMATION: fusion sequence
US-10-267-311-53
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LENGTH: 647
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTON: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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Best Local Similarity
                                                                                                                                                                                                                                                          APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 99.0%;
Local Similarity 96.9%;
les 95; Conservative
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Pred. No. 1.9e-52;
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                                                                                                                                                                                                                                                                                                                   RESULT 55
US-10-530-253-3
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TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-5
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Best Local Similarity
Matches 95; Conserv
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Publication No. US20060014926A1
GENERAL INFORMATION:
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Publication No. US20060014926A1
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PRIOR FILING DATE: 2003-10-02
PRIOR PPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
                                                   APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
PILE REPERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
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APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhine
                                                                                                                                                                                                          APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 98.8%; Local Similarity 95.9%;
               APPLICATION NUMBER: US 60/415,929
FILING DATE: 2002-10-03
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Pred. No. 1.9e-52;
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GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
ITITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: TBA
CURRENT APPLICATION NUMBER: US/10/201,764
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/566,420
PRIOR FILING DATE: 2000-05-05
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LENGTH: 248
TYPE: PRT
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SOFTWARE: PatentIn versi
SEQ ID NO 3
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                                                                                                                                                                                          Sequence 19, Application US/10201764
Publication No. US20030166140A1
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Best Local Similarity
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Best Local
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                          151 LHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 210
                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                  61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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95.9%;
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    Mismatches

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Pred. No. 1e-52;
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Pred. No. 1.3e-52;
1; Mismatches 3
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                                                                                                                                  FOR ANTIGENS WHICH ELICIT AN
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; PRIOR FILING DATE: 1999-05-06; PRIOR APPLICATION NUMBER: 60/132,750; PRIOR FILING DATE: 1999-05-06; NUMBER OF SEQ ID NOS: 19; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 19; SEQ ID NO 19; LENGTH: 98; TYPE: PRT; ORGANISM: Human papillomavirus type E7US-10-201-764-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
ITITLE OF INVENTION: IMMUNE RESPONSE
ITILE OF INVENTION: IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/10/681,410
CURRENT FILING DATE: 2003-10-08
PRIOR APPLICATION NUMBER: US/10/201,764
PRIOR APPLICATION NUMBER: US/9566,420
PRIOR FILING DATE: 2002-07-22
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 19
                                                                                                                                        US-10-484-063-26
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; TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-681-410-19
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Sequence 26, Application US/10484063
Publication No. US20050048467A1
GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLEKO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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Best Local !
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Similarity 95.9%;
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95.9%;
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Pred. No. 7.4e-53;
1; Mismatches 3
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Pred. No. 7.4e-53;
1; Mismatches 3
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    HPV-ASSOCIATED
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RESULT 61
US-10-392-113-29
; Sequence 29, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
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SEQ ID NO 26
LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus type
US-10-484-063-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
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US-10-472-724-4
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Publication No. US20040171806A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILLING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2010-7-20
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: UTSC:560US
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 111
                                                                                                                                                                                                                                                                                                             Local Similarity 96.9
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                                                                                                                                               DSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                              HGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKC
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96.9%;
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                                                                                                                                                                                                                                                                                                             Score 507; DB 4; I
Pred. No. 8.6e-53;
0; Mismatches 3;
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Pred. No. 7.4e-53;
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                                                                                                                                               103
                                                                                                                                                                                                                                                                                                                                                     Length 111;
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GENERAL INFORMATION:

APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RES
FILE REFERENCE: 12071/002001
CURRENT APPLICATION UNMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/9/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
PRIOR MATTON: Fusion Sequence
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US-10-267-311-8
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 45
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 98
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Best Local Similarity
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TITLE OF INVENTION: OF CANCER CELLS
FILE REFERENCE: 21108.0005U3
CURRENT APPLICATION NUMBER: US/10/392,113
CURRENT FILING DATE: 2003-03-17
ERIOR APPLICATION NUMBER: 60/365,078
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
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                                                                                                                                                                                                                                                                                                                                                      Match 97.3%;
Local Similarity 95.9%;
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                                                                                                                                                                                                        1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                      MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                           Score 503; DB 4; Length 98; Pred. No. 2.2e-52;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
FIILE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
FRIOR APPLICATION NUMBER: US/99/613,303
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 29
LEWITH: 648
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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                                                                                                                   Query Match
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/00/613,303
PRIOR PELICATION NUMBER: US/09/613,303
PRIOR PELICATION NUMBER: US/09/613,303
PRIOR PELICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1909-07-08
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                              Local
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                                                                                              Similarity
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MHGDTFTLHEYMLDLQPETTDLYXXXQLNDSSEEBBIDGPAGQAEPDRAHXNIVTFCCK 60
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                                                                     97.3%;
llarity 95.9%;
Conservative
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Pred. No. 2.2e-52;
0; Mismatches 4
                                                                     Score 503; DB 4; Length 648; Pred. No. 2.3e-51; O; Mismatches 4; Indels
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
FILE CANT: Mizzen, Lee A.
FILE REFERENCE: 12071/002001
CURRENT APPLICATION UMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-08
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
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US-10-267-311-41
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US-10-679-956-29
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 Query Match
                                                                                                                      SEQ ID NO 41
LENGTH: 711
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Publication No.
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Best Local (
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
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APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
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APPLICANT: Chu,
APPLICANT: Mizze
                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                  ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                 OTHER INFORMATION: fusion sequence
                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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 97.38;
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 Score 503;
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2.3e-51;
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Length 711;
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                                                                                                                                                                                                                                                                                                                                                                       RESULT 68
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                                  ENGTH:
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APPLICANT: Siegel, Marvin
APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RES
FILE REFERENCE: 12071/002001
CURRENT APPLICATION UNMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: fusion sequence US-10-679-956-41
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/10267311 Publication No. US20030050469A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 711
                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/10679956 Publication No. US20050089841A1
                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                              APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
                                                                                                                        NUMBER OF SEQ ID NOS:
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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Pred. No. 2.6e-51;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
FILE REFERENCE: 12071/002001
FILE REFERENCE: 12071/002001
FILE REFERENCE: 12071/002001
FILE OF ILING DATE: 2003-10-06
FRIOR APPLICATION NUMBER: US/09/613,303
FRIOR FILING DATE: 2000-07-10
FRIOR FILING DATE: 1999-07-08
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US-10-115-440-7
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; OTHER INFORMATION:
US-10-267-311-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10115440 Publication No. US20040086845A1 GENERAL INFORMATION:
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Best Local 9
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Best Local Similarity
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APPLICANT: WU, TZYY-Choou
APPLICANT: HUNG, Chien-Fu
TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF J
TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN
FILE REPERENCE: 02240-179934
CURRENT APPLICATION NUMBER: US/10/115,440
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 60/281,003
PRIOR APPLICATION NUMBER: US 60/281,003
PRIOR APPLICATION NUMBER: PCT/US00/41422
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: PCT/US00/41422
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/501,097
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94; Conservative
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Vo. US20050089841A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 503; DB 5;
Pred. No. 2.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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RESULT 72

US-11-072-288-2

Sequence 2, Application US/11072288
Publication No. US20050159386A1
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine

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US-10-115-440-5
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/281,003
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/US00/41422
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/501,097
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/421,608
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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                                                                                                                                               Matches
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                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN FILE REFERENCE: 02240-179934 CURRENT APPLICATION NUMBER: US/10/115,440 CURRENT FILING DATE: 2002-09-30 CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-10-20 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                        LENGTH: 28
TYPE: PRT
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                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
234
                                                                       174 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 233
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                                                                                                          1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
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                                                                                                                                             Conservative
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Pred. No. 5.2e-52;
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Pred. No. 1.9e-51;
                                                                                                                                               Mismatches
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269
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APPLICANT: Jeffrey K. Fullen
APPLICANT: Susan P. McElhiney
FILE OPTINENTION: HUMAN PAPILLOWAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT FILING DATE: US/10/530,253
CURRENT FILING DATE: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US/10/301726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-03
INUMBER: OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
US-10-530-253-30
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US-11-072-288-2
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CURRENT APPLICATION NUMBER: US/11/072,288
CURRENT TILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US/09/462,993
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhine
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Publication No. US20060014926A1
                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                     Similarity
               KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSS-EEEDEIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETT-----QLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                             MHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC 60
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                 73.8%;
73.5%;
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%; Pred. No. 9.4e-38;
11; Mismatches 14
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Pred. No. 5e-49;
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US-10-530-253-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 29
LENGTH: 97
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APPLICANT: Cassetti, Maria C.

APPLICANT: Smith, Larry

APPLICANT: Smith, Larry

APPLICANT: Susan P. McElhiney

TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS

FILE REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M137-US2

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FULE REFERENCE: 0630/100M137-US2

FUL REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M137-US2

FULE REFERENCE: 0630/100M13
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SEQ ID NO 28
LENGTH: 98
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                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Publication No. US20060014926A1
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APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ. ID NOS: 65
NUMBER OF SEQ. ID NOS: 65
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Best Local Similarity
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                       56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRGETPTLQDYVLDLQPEAIDLHCYEQLPDSSDEEDVIDSPAGQAEPDTSNYNIVTFCCQ
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                       MRGHKPTLKEYVLDLYPEPTDLYCYEQLSDSSDEDEGLDRPDGQAQPATADYYIVTCCHT 60
                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                  57.1%; Score 295; DB 5; 57.7%; Pred. No. 2.3e-27;
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Pred. No. 1.3e-36;
2; Mismatches 16
                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                    Length 97;
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APPLICANT: CASSETI, MARIA C.
APPLICANT: GASSETI, MARIA C.
APPLICANT: Smith, Larry
APPLICANT: Susan p. McElhiney
ITITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 98
TYPE: PRI
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; ORGANISM: Human papillomavirus type 52
US-10-530-253-34
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Best Local Similarity 5/...
56; Conservative
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 99
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Publication No. US20060014926A1
                                                                            Matches
                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: WS 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                           ORGANISM: Human papillomavirus type 58-10-530-253-36
                                                                                                    Local
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1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEED-EIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRGDKATIKDYILDLQPETTDLHCYEQLGDSSDEEDTDGVDRPDGQAEQATSNYYIVTYC 60
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                                                                                                      Similarity
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CNTTVRLCVNSTASDLRTIQQLLMGTVNIVCPTCAQQ 97
                                                                          56.0%; Score 289.5; DB 5; llarity 57.1%; Pred. No. 1.1e-26; Conservative 16; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.9%; Score 294; DB 5; Length 99; 57.1%; Pred. No. 3.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                        Length 98;
                                                                            Indels
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                                                                            Gaps
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GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.

APPLICANT: Chicz, Roman M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPTIOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

CURRENT FILING DATE: 2004-01-05

PRIOR APPLICATION NUMBER: US/0/664,225

PRIOR APPLICATION NUMBER: US 60/169,846

PRIOR APPLICATION NUMBER: US 60/169,846

PRIOR APPLICATION NUMBER: US 60/154,665

PRIOR APPLICATION NUMBER: US 60/154,665

PRIOR APPLICATION DATE: 1999-10-16
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US-10-751-845-126
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US-10-367-057-12
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                                                                ; OTHER INFORMATION: Artificial US-10-751-845-126
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; ORGANISM: Homo sapiens
US-10-367-057-12
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SOFTWARE: CUraSeqList version 0.1
SEQ ID NO 12
LENGTH: 98
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APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods
FILE REFERENCE: 21402-559
                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 126, Application US/10751845 Publication No. US20050100928A1
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Query Match
Best Local Similarity
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CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                       LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHGDTPTLHEYMLDLQ-PETTDLYXYXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHGRLVTLKDIVLDLQPPDPVGLHCYEQLEDSSEDEVDKVD--KQDAQPLTQHYQILTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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41.6%;
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Score 215; DB 5;
Pred. No. 1.2e-17;
                                                                                       fusion sequence
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                  Length 117;
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APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
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US-10-751-845-158
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SEQ ID
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CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Artificial fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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Local Similarity 52.2%;
les 48; Conservarion
NO 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
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                     FastSEQ for Windows Version 4.0
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o. US20050100928A1
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o. US20050100928A1
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Pred. No. 3e-17;
0; Mismatches 2
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RESULT 83
US-10-530-253-32
J Sequence 32, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
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APPLICANT: Cirban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING PO-
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/9/664,225
PRIOR APPLICATION NUMBER: US/9/664,225
PRIOR PILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
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US-10-751-845-160
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LENGTH: 261
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Best Local Similarity
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Best Local Similarity
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McBlhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
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SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                          -----LLMGTLGIVCPICSQKP
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Pred. No. 3.3e-17;
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Pred. No. 3e-17;
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RESULT 84
US-10-433-091-4
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US-10-530-253-32
                                                                                                                                               RESULT 85
Sequence 27, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassecti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
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Publication No. US20040101533A1
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Best Local (
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APPLICANT: NIELAND, JOHN
APPLICANT: GABELSBERGER, JOSEF
APPLICANT: HERBST, RUTH
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NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 100 59 630.4 PRIOR FILING DATE: 2000-12-01 NUMBER OF SEQ ID NOS: 72 SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 41.2%; Score 213; DB 5; Local Similarity 43.8%; Pred. No. 1.9e-17;
                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                 52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
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                                          US-10-899-771-19
                                                              RESULT 87
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TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 0630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR PPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 105
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Sequence 19, Application US/10899771 Publication No. US20050031638A1
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                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human papillomavirus type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                               114 MHGPKATLQDIVLHLEPQNEIPVDLLGHQQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                 172
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                                                                                                                                                                  52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPET---TDLYXXXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
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                                                                                                                               HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ 217
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39.6%; Pre-
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                                                                                                                                                                                                                                                                                                 Score 201.5; DB of Pred. No. 1.2e-15, O; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                           Length 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 88
US-10-000-903-23
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                                                                                                                                                                     ; ORGANISM: Homo sapien 
US-10-000-903-23
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Appropriate Publication No.
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                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva,
APPLICANT: Delisse, Anne-M
APPLICANT: Gerard, Catheri
APPLICANT: Lombardo-Benche
                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/000,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions Comprising Human PaTITLE OF INVENTION: and Fusion Proteins Adjuvanted FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 227
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                      1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                  42;
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MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR-- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                                  Conservative
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                                                                              38.8%; Score 200.5; DB 4; 39.6%; Pred. No. 3e-15; tive 20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 201.5; DB 5
Pred. No. 1.2e-15;
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juvanted with a CpG Oligonucleotide
                                                                                                                      DB 4;
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                                                                                                                         Length 383;
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TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
TITLE OF INVENTION: of the Immune Response Therefrom
FILE REFERENCE: 600-1-081CONCIP1
CURRENT APPLICATION NUMBER: US/10/800,023
CURRENT FILING DATE: 2004-03-14
PRIOR APPLICATION NUMBER: 09/925,284
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/986,704
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: PCT/US96/01383
PRIOR FILING DATE: 1996-01-31
PRIOR APPLICATION NUMBER: 08/381,528
PRIOR APPLICATION NUMBER: 08/381,528
PRIOR FILING DATE: 1995-01-31
PRIOR FILING DATE: 1995-01-31
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US-10-899-771-23
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US-10-800-023-28
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
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SEQ ID NO 23
LENGTH: 383
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APPLICANT: Steinman, Ralph
APPLICANT: Nussenzweig, M
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Publication No. US20040258688A1
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and B6E7 fusion from Human papilloma OTHER INFORMATION: virus type 18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 373
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Bonifaz, Laura
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; ORGANISM: human papilloma virus E7 protein
US-10-800-023-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 92
US-10-530-253-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human Papillomavirus E7
US-11-041-893-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MAHAIRAS, Gregory G.
APPLICANT: MAHAIRAS, Gregory G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
FILE REFERENCE: 100123,401
CURRENT APPLICATION NUMBER: US/11/041,893
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/616,855
PRIOR PILING DATE: 2004-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 42; Conserv
                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/10530253 Publication No. US20060014926A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No.
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2002-10-03
                                                                                                                                                                                                                                                        APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 295
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                      NUMBER OF SEQ ID NOS: 65
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ORGANISM: Human papillomavirus type 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 35
                                           ENGTH: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 GQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIR 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.9%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.4%;
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Pred. No. 1.1
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. 1.1e-15;
tches 33;
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; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8
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US-10-472-724-8
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                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10000903 Publication No. US20020182221A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10472724
Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
                                                       FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
                                                                                                                                                                                                                 APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                     APPLICANT: Bruck, Claudine APPLICANT: Cabezon Silva,
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                   TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Modified HPV E6 and E7
FILE REFERENCE: 4121-154
                                          PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 NIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--H 64
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; Pred. No. 2.5e-15
17; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 195.5; DB 4;
Pred. No. 2.8e-15;
20: Mismatches 33;
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US-10-899-771-16
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US-10-000-903-16
                                                                                                                          Sequence 35, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/10899771 Publication No. US20050031638A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Swith, Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR PILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E7 from Human papilloma virus OTHER INFORMATION: 18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 227
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
REFERENCE:
                                                                                                                                                                                                                                                                                        172 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDEVNHQHLPARRAEPQR-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 37.2%; al Similarity 38.7%; 41; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                   1 MHGDTPTLHEYMLDLQPET----TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MHGDTPTLHEYMLDLQPET---TDLYXXYQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                  YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                              MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDEVNHQHLPARRAEPQR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.2%; Score 192.5; DB 5; 38.7%; Pred. No. 1.4e-14;
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Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus type
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RESULT 98
US-10-530-253-31
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US-10-530-253-33
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                                                          Sequence 31, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10
TYPE: PRT
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LIHVPCCECKFVVQLDIQSTKEDLRVVQQLLMGALTVTCPLCA 102
                                                                                                                                                                                                       6
                                                                                                                                                                                                                                         56 TFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXFICS 95
                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 NIVTECCKCDSTLRLCVQSTHVDIRTLEDILMGTLGIVXPICS 95
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                                                                                                                                                                                                     APCCRCSSVVQLAVESSGDTLRVVQQMLMGELSLVCPCCA
                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPET-TDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH----YNIV 55
                                                                                                                                                                                                                                                                                     MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGKVPTLQDVVLELTPQTEIDLQCNEQL-DSSEDEDEDEVDHLQERPQQARQAKQHTCY
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      34.4%;
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                                                                                                                                                                                                                                                                                                                                                               Score 178; DB 5; L
Pred. No. 2.9e-13;
Midmatches 37;
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Pred. No. 2.7e-13;
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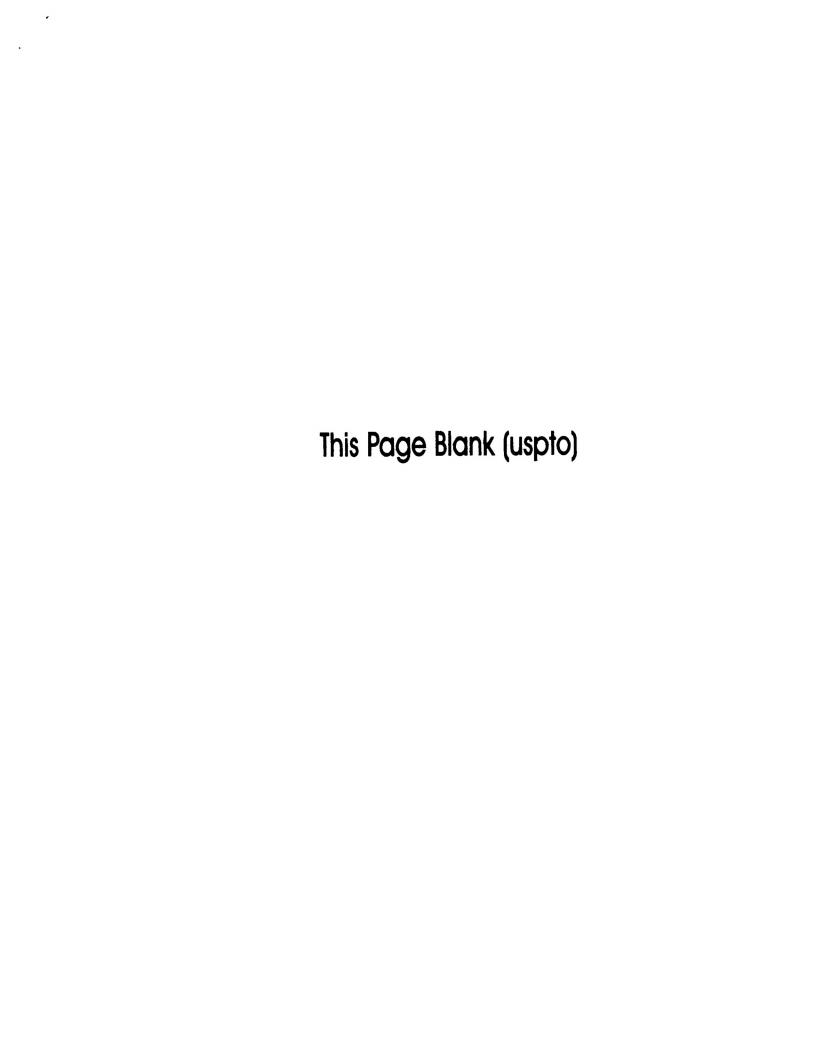
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Sequence 38, Application US/10530253

Publication No. US20060014926A1

GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
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; TYPE: PRT
; ORGANISM: Human papillomavirus type 68
US-10-530-253-38
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US-10-530-253-38
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US-10-475-203A-14
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; TYPE: PRT
; ORGANISM: Human papillomavirus type 39
US-10-530-253-31
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PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
Sequence 14, Application US/10475203A Publication No. US20040241177A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.8%; Score 164.5; DB 5; Best Local Similarity 34.0%; Pred. No. 1.4e-11; Matches 36; Conservative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
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                                                                                                                                                                                                                        50 AHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 EPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Conservative
                                                                                                                                                                         61 QRHRIQCICCKCNKALQLVVEASRDNLRTLQQLFMDSLNFVCPWCA 106
                                                                                                                                                                                                                                                                                                                         1 MHGDTPTLHEYMLDLQP----ETTDLYXYXQLNDSSEEEDEIDGPAGQAE------PDR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRGPKPTLQEIVLDLCPYNEIQPVDLVCHEQLGES---EDEIDEPDHAVNHQHQLLARRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%; Score 170; DB 5 39.1%; Pred. No. 3e-12;
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                                                                                                                                                                                                                                                                                                                                                                        Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 110;
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; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: INFORMATION: Polypeptide encoded by SEQ ID NO: US-10-475-203A-14
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: AU PR4468/01
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/475,203A
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/AU02/00486
PRIOR FILING DATE: 2002-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRAZER, IAN
TITLE OF INVENTION: NOVEL COMPOSITIONS AND USES THEREFOR
FILE REFERENCE: E1679-00002
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 517
489
                                                                                 429 EKEKPDPYKNISFWEVNIKEKFSSELDQYPLGRKFILQSHGHFQIVTCCCGCDSNVRLVV
                                       70 QSTHVDIRTLEDLIMGTLGIVXPICSQK 97
                                                                                                                         16 QPETTDLY---XYXQLNDSSEEEDEIDG-PAGQ--AEPDRAHYNIVTFCCKCDSTLRLCV 69
QCTETDIREVQQLLLGTLNIVCPICAPK 516
                                                                                                                                                                      Conservative
                                                                                                                                                                   30.2%; Score 156; DB 5; 1
40.9%; Pred. No. 9.7e-10;
ative 13; Mismatches 33;
                                                                                                                                                                                                           Length 517;
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Search completed: May 27, 2006, 05:37:53 Job time: 103.936 secs



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Result
No.
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Maximum
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Perfect
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0
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Query
Match
                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA_New:*

1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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1 MHGDTPTLHEYMLDLQI
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US-10-511-814-11
Sequence II, Application US/10511814
Publication No. US20060088472A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
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Publication No. US20060088472A1
GENERAL INFORMATION:
  Query Match
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Best Local
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APPLICANT: Mcstbrook, III, Thomas F.
APPLICANT: Westbrook, III, Thomas F.
APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: ET REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEG ID NOS: 21
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/511,814
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
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APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1)
FILE REFERENCE: 21108.0016U2
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                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                              OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
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l Similarity 96.9%;
95; Conservative
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878
  98.8%;
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US-11-293-697-3814
  Score 511;
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Length 98;
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Sequence 3814, Ap
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APPLICANT: Jacquet, Alain
APPLICANT: Bollen, Alex
TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: COMPRISING IT AND ITS PREPARATION PROCESS
FILE REFERENCE: 9997.50USWO
CURRENT APPLICATION NUMBER: US/10/512,190
CURRENT APPLICATION NUMBER: PCT/BE03/000073
PRIOR APPLICATION NUMBER: PCT/BE03/000073
PRIOR APPLICATION NUMBER: US 60/410,461
PRIOR APPLICATION NUMBER: US 60/410,461
PRIOR APPLICATION NUMBER: PCT/BE03/000073
PRIOR APPLICATION NUMBER: FR 0205173
PRIOR APPLICATION NUMBER: FR 0305173
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 9
SOFTMARE: Patentin version 3.3
US-11-293-697-2678

Sequence 2678, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
FILE OF INVENTION: NOVel full length cDNA
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTMARE: Patentin Ver. 2.1

SEQ ID NO 2678
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Matches 94; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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1; Mismatches
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Pred. No. 1.3e-46;
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US-11-293-697-4473; Sequence 4473, Application US/11293697; Publication No. US20060105376A1; GENERAL INFORMATION:
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US-10-505-928-341
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                                                                         ) ORGANISM: Homo sapiens
US-11-293-697-4473
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Query Match 11.6%;
Best Local Similarity 22.7%;
Matches 29; Conservative 1
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                                                                                                                                             SEQ ID NO 4473
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Best Local Similarity
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                            PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                         APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                          FILE REFERENCE: H1-A0106
                                                                                                             LENGTH: 4
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llarity 30.6%;
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 ; Score 60; DB 7; Length 468; ; Pred. No. 16; 17; Mismatches 30; Indels
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 39521
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US-10-953-349-39521
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US-10-953-349-39520
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Publication No. US20060107345A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.3 SEQ ID NO 39520
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Best Local Similarity
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Best Local
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al. TITLE OF INVENTION: SEQUENCE-DETERMINED TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                        LENGTH: 616
                                                                                          Local
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505 PAVHMASVDLKGKAYDV-----LRQNSSRFLLEDVYRNPGPLQFEGPGADSKP-----
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                                                                                            Similarity
                                 PTLHEYMLDLQPETTDLYXYXQLNDSSEE---ED-----EIDGPAGQAEPDRAHYNI 54
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                                                                        Conservative
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                                                                      Score 58.5; DI
Pred. No. 32;
LS; Mismatches
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Pred. No. 23
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APPLICANT: ALEXANDROV, Nickolai et al.
FITTLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FITTLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 39519
LENGTH: 646
TYPER: PRT
ORGANISM: Zea may8 subsp. may8
US-10-953-349-39519
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US-10-953-349-39519
J. Sequence 39519, Application US/10953349
J. Publication No. US20060107345A1
J. GENERAL INFORMATION:
                                                                                                                           RESULT 11
US-10-953-349-27425
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Sequence 27425, Application US/10953349
publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE DETERMINE
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27426
LENGTH: 233
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publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Triticum aestivum
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                                                                                                                                                                                                                                                       8 LHEYML-DLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDST 64
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SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES ENCONDED THERBY
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27.6%; Pred. No. 14;
tive 11; Mismatches
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Pred. No. 33;
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 27424
LENGTH: 353
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-953-349-27424
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CURRENT FILING DATE: 2004-09-30;
NUMBER OF SEQ ID NOS: 40252;
SOPTWARE: PatentIn version 3.3;
SEQ ID NO 27425;
LENGTH: 296;
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-953-349-27425
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US-10-953-349-39537
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US-10-953-349-27424
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PACENTIN VERSION 3.3
SEQ ID NO 39537
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39537, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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Best Local Similarity 27.6%;
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TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
                                                                                                                                                                                                                                                                                                                APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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                                                                                                                                                                             LENGTH: 446
TYPE: PRT
                                                                             Local Similarity
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Local Similarity 27.6%;
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6 PTLHEYMLDLQPETTDLYXYXQLNDSSEEED---
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                                                             Conservative
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                                                                           11.1%; Score 57.5; 23.8%; Pred. No. 29;
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                      ----EIDGPAGQAEPDRAHYNIVTF 57
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RESULT 14
US-10-953-349-39536
US-10-953-349-39536
Sequence 39536, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
GENERAL INFORMATION: Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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US-10-953-349-39536
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US-10-953-349-3780
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                    Sequence 3780, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2004-09:
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3781
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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CURRENT APPLICATION NUMBER: US/10/953,349
APPLICANT: ALEXANDROV, Nickolai et al.
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                                                                                                                                                                                              LNDDDDDDDDCDW-----EPVQAPMEFVKWCCVNCTMSNPGDMVHCCICGEH 59
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Pred. No. 33;
8; Mismatches
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Pred. No. 30;
15; Mismatches
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CURRENT APPLICATION NUMBER: US/11/242,111
CURRENT FILING DATE: 2005-09-29
PRIOR APPLICATION NUMBER: 60/614,746
PRIOR FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: 60/651,344
PRIOR FILING DATE: 2005-02-08
NUMBER OF SEQ ID NOS: 64
SOPTWARE: Patentin version 3.3
SEQ ID NO 23
LENGTH: 300
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US-10-953-349-39535
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                                                                                                                                                                                                                                                                                                                                                                                     US-11-242-111-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: PAtentin version 3.3 SEQ ID NO 3780 LENGTH: 552 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39535, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30

CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version
SEQ ID NO 39535
LENGTH: 618
                                                                                                                                                                                                                          Sequence 23, Application US/11242111
Publication No. US20060088862A1
GENERAL INFORMATION:
APPLICANT: Lee, Nancy M
TITLE OF INVENTION: OR COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
FILE REFERENCE: NLEE-01001US1 MCF/MLB
FILE REFERENCE: NLEE-01001US1 MCF/MLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 ----ISLCVEDQDYMGRIKKLQEYLEKVKRIVKPGCSQ 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 CCKCDSTLRLCVQSTHV--DIRTLEDILMGTLGIVXPICSQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LNDDDDEDDDCDW-----EPVQAPMEFVKWCCVNCTMSNPGDMVHCCICGEH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LNDSSEBEDEIDGPAGQAEPDRAHYNIVTFCC-KCDST-----LRLCVQSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PTLHEYMLDLQPETTDLYXXXQLNDSSEEED-----EIDGPAGQAEPDRAHYNIVTF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.5;
Pred. No. 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 552;
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 23406
LENGTH: 286
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-953-349-23406, Application US/10953349; Sequence 23406, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: HUMAN
US-11-242-111-23
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US-09-981-845-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09981845 Publication No. US20060105013A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ashkar, Samy
IITLE OF INVENTION: Osteopontin-Coated Surfaces and Methods of
FILS REFERENCE: CMCC 779
CURRENT APPLICATION NUMBER: US/09/981,845
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,248
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
PRIOR PPLICATION NUMBER: US 60/327,273
PRIOR PPLICATION NUMBER: US 60/327,273
PRIOR FILING DATE: 2001-110-05
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Children's Medical Center Corporation APPLICANT: Ashkar, Samy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 11.0%; Score 57; DB Local Similarity 24.4%; Pred. No. 21;
188 KVDGPGGWSYGIKVRYSVQGNDEFCGACEATAGTC 222
                                        37 EIDGPAGQAEPDRAHYNIV---TFCCKCDSTLRLC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 HDHMDDMDDEDDDDHVDSQDSIDSNDSDDVDDTDDSHQSDESHHS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 HEYMLDLOPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYN 53
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                                                                                      Conservative
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                                                                                                        Score 55.5;
Pred. No. 30;
                                                                                      Mismatches
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                                                                                                                            DB 6;
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                                                                                    14;
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CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5452
LENGTH: 538
TYPE: PRT
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US-10-953-349-5451
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                                                                                                                                                  Sequence 5451, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 23405
LENGTH: 293
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                APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETENHED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FAPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
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CURRENT FILING DATE: 2004-09-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                                                                                                                                                                                                                     149 DEEPE----HDAFRLPTEEELEEEARGP-----PDLPLLKTRIEEIVRALKNFKAFRPK- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 KVDGPGGWSYGIRVRYSVQGNDEFCGACEATAGTC
                                                                                                                                                                                                                                                                                                                          62 DSTLRLCVQSTHVDIRT---LEDLLMGTLGIVXP 92
                                                                                                                                                                                                                                                                                                                                                                                                         14 DLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPD------RAHYNIVTFCCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 EIDGPAGQAEPDRAHYNIV---TFCCKCDSTLRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                          DTTRKACVEQLKADLGSYYGYNSFLIGTLVEMFP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 55.5;
27.7%; Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Sequence 32, Application US/10468193
; Publication No. US20060100416A1
; GENERAL INFORMATION:
   APPLICANT: Palli, Subba R.
; APPLICANT: Cress, Dean E.
; APPLICANT: Kumar, Mohan B.
; TITLE OF INVENTION: Receptor-Based Inducible Gene Expression System
; FILE REFERENCE: A01247-US
; CURRENT APPLICATION NUMBER: US/10/468,193
; CURRENT APPLICATION NUMBER: US 60/313,925
; PRIOR APPLICATION NUMBER: DCT/US02/05090
; PRIOR APPLICATION DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: DCT/US02/05090
; PRIOR APPLICATION NUMBER: DCT/US02/05090
; PRIOR APPLICATION NUMBER: 2002-02-20
; NUMBER OF SEQ ID NOS: 113
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US-10-468-193-32
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US-10-953-349-5450
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US-10-953-349-5450
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 5450
LENGTH: 574
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LENGTH: 544
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTTRKACVEQLKADLGSYYGYNSFLIGTLVEMFP 268
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27.7%; Pred. No. 63;
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; ORGANISM: Drosophila melanogaster
US-10-468-193-32
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US-10-525-126-215
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Publication No. US2006093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 177
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APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
                                                           SOFTWARE: PatentIn Ver. 3.2 SEQ ID NO 215
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Publication No.
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                                                                                                                         CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
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CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
                                                                                               PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
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ORGANISM: Unknown Organism
FEATURE:
ORGANISM: Salmo salar
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les 10; Conserv
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27; Conserv
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24.8%; Pred. No. 1
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Pred. No. 6.
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US-10-525-126-174
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TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REPERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT APPLICATION NUMBER: PCT/CA03/01323
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: RAPELICANT: NATIONAL RESEARCH COUNCIL OF CANADA TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH FILE REFERENCE: 6899-6/PAR
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    Query Match
                                                                                                                                                                                         SEQ ID NO 175
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                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
                                                                                                            TYPE: PRT
ORGANISM: Unknown Organism
                                                                OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide OTHER INFORMATION: sequence
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ORGANISM: Unknown Organism
                                                                                                         FEATURE:
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                                                                                                                                                                      LENGTH: 88
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                                                              Description of Unknown Organism: Hepcidin peptide sequence
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Pred. No. 6
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Pred. No. 1
  Score 54.5;
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  DB 6;
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FILE REFERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
PRIOR PILING DATE: 3.2
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 212
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US-10-525-126-212
                                                                                                          US-10-525-126-213
                                                      Matches
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Matches 10; Conservative
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TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
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les 10; Conserv
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                          32 SEEEDEIDGPAGQAEPD-----------RAHYNIVTFCCKC 61
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                                                                   Similarity
TEEVESIDSPYGEHOOPGGTSMNLPMHFRFKROSHLSLCRWCCNC
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o. US20060093596A1
                                                      Conservative
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Pred. No. 11;
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Pred. No. 11;
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                                                                                                           US-10-525-126-300
                                                                                                                                RESULT 34
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                  Sequence 300, Application No. US200 GENERAL INFORMATION: APPLICANT: NATIONAL
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTINICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 299
LENGTH: 88
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SEQ ID NO 284
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Best Local (
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CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
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CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
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TYPE: PRT
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o. US20060093596A1
                                                            Application US/10525126
D. US20060093596A1
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llarity 22.2%;
Conservative
RESEARCH COUNCIL OF CANADA A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
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Pred. No. 11;
9; Mismatches
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Pred. No. 11;
9; Mismatches
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 20549
LENGTH: 255
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-20549
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                                                                                                        Sequence 20548, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SECOUBLE THERBY
PILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 20548

TENCTY: 326
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NUMBER OF SEQ ID NOS: 329
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 300
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
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CURRENT FILING DATE: 2005-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Salmo salar
                                                        ORGANISM: Glycine max
                                                                               TYPE: PRT
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Pred. No. 11;
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Length 269;
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Query Match

10.5%;

Score 54.5;

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US-11-293-697-2988
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US-11-293-697-2988
                                                                                                                                                                                                                                                                            APPLICANT: ALEXANDROV, NICKOIAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1526
LENGTH: 278
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1526, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVel full length cDNA
FILE REFERENCE: H1-A0106
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Publication No. US20060105376A1
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LENGTH: 489
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                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana -10-953-349-1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/293,697 CURRENT FILING DATE: 2005-12-05 PRIOR APPLICATION NUMBER: US/10/108,260 PRIOR FILING DATE: 2002-03-28 NUMBER OF SEQ ID NOS: 5458 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                           0.4%; Score 54; DB (Local Similarity 27.4%; Pred. No. 42; Local Similarity 27.4%; Pred. No. 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AQQLTHIELDRVSSIYPEDLM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 LQELREKLRPPAVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 HNPNPNAKAVKFDI-PEEDDDYTDDELDDFDDDDDDDDDDDEFDDDEMD 153
                                     67 LCVQSTHVDIRTL 79
                                                                             62 TLNEPTIGDKLESLDLLNGEKVN--SEESNRDSAPGDDKPPTAASVNV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 CVQSTHVDIRTL----EDLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                 7 TLHEYMLDLOPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 HGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPD
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LLRQALHADDRSL 120
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24.7%; Pred. No. 69;
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                                                                                                                                                           29; Indels
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Sequence 35808, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 35808
LENGTH 630
LENGTH: 630
LENGTH: 630
LENGTH: 630
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US-10-953-349-35808
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                                                                                                                                                                       Matches
                                                                                                                                                                                                             Query Match
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APPLICANT: Maarten van den Brink, Johannes
APPLICANT: Harboe, Marianne K
APPLICANT: Harboe, Marianne K
APPLICANT: Petersen, Steen Guldager
APPLICANT: Rahbek-Nielsen, Henrik
TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE POLYPEPTIDE IN
TITLE OF INVENTION: A RECOMBINANT HOST ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PA 2002 0092 PRIOR FILING DATE: 2002-06-17 NUMBER OF SEQ ID NOS: 8
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CURRENT FILING DATE: 2004-12-17
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TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                         Local
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tes 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VF----DNMMNRHLVAQDLFSVYMDRNGQESML--TLGAIDP 173
86
                                                                                  32 VELRAETDSDEVYAQIMLQPQTEQSEPTSPDPEPPEPERC--NIHSFC---
                                        71 STH 73
                                                                                                                        13 LDLQPET--TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 TFCCKCDSTL--RLCVQ---STHVDIRTLEDLLMGTLGIVXP 92
                                                                                                                                                                     l Similarity
18; Conserv
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STH 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVIVSN-IVDIOQTVGLSTQEPGDVFTYA---
                                                                                                                                                                  10.4%; Score 54; DB 6; ilarity 28.6%; Pred. No. 1e+02; Conservative 10; Mismatches 2
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                                                                                                                                                                                                             Length 630
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                                                                                                                                                                       Indels
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                                                                                    -KTLTASDT 85
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RESULT 41 US-10-953-349-35807 ; Sequence 35807, Application US/10953349

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RESULT 42
US-10-953-349-31198
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; Sequence 23351, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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US-10-953-349-35807
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 35807
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 31198
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Publication No. US20060107345A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version:
SEQ ID NO 23351
LENGTH: 639
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Best Local Similarity
                                                                            APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 533
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
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Sequence 23350, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOTTWARE: PatentIn version 3.3
SEQ ID NO 23350
LENGTH: 656
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                             Sequence 23349, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 23349
LENGTH: 664
                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Glycine max US-10-953-349-23349
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US-10-953-349-23349
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US-10-953-349-23350
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                                                             RESULT 46
US-10-953-349-34172
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Best Local S
Matches 16
Sequence 34172, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                        Query Match 10.3%;
Best Local Similarity 27.1%;
Matches 16; Conservative
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                                                                                                                                           44 EEEEEEEEVWDDWEGEDEGERESEFVCLFCDSRYSSCGSLFDHCASLHRFDFHTIRTTL 102
                                                                                                                                                                                  30 DSSEEEDEI-DGPAGQAEPDRAHYNIVTFC----CKCDSTLRLCVQSTHVDIRTLEDLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 EEEEEEEVWDDWEGEDEGERESEFVCLFCDSRYSSCGSLFDHCASLHRFDFHTIRTTL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 DSSEEEDEI-DGPAGQAEPDRAHYNIVTFC----CKCDSTLRLCVQSTHVDIRTLEDLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 EEEEEEEVWDDWEGEDEGERESEFVCLFCDSRYSSCGSLFDHCASLHRFDFHTIRTTL 77
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Pred. No. 1.2e+02;
7; Mismatches 31;
                                                                                                                                                                                                                        Score 53.5; DB 6;
Pred. No. 1.2e+02;
7; Mismatches 31;
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Pred. No. 1.2e+02;
7; Mismatches 31;
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34170
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15798US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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US-10-953-349-34170
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US-10-953-349-34171
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PAPPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34172
LENGTH: 263
TYPE: PRT
                                                                                                                                                            Sequence 34170, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 34171
LENGTH: 283
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Best Local (
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25; Conservative
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 12021
LENGTH: 377
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; TYPE: PRT
; ORGANISM: Zea mays subsp.
US-10-953-349-34170
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The Local Similarity
The Conservation
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Best Local Similarity
                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (325)...(325) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                       LOCATION: (314)..(314)
OTHER INFORMATION: Xaa
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LOCATION: (314)..(314)
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NAME/KEY: misc feature
LOCATION: (252)..(252)
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OTHER INFORMATION: Xaa
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LOCATION: (224)..(224)
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LGVPLP 157
                            LGIVXP 92
                                                           TEWELDFCSRPILDARGKKVWELVVCDKTLSL--QYTKYFPNNVINSITLKDAIVAVSDQ 15:
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                                                                                                                                                        TPT-LHEYMLDLQPETTDLYXYXQL-----NDSSEEEDEIDGPAGQ-----AEPDRA
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Pred. No.
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Pred. No. 56;
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RESULT 50 US-11-293-697-3292

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FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2002-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3292

LENGTH: 423
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US-10-953-349-15959
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US-11-293-697-3292
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SOPTWARE: PatentIn 3.2
SEQ ID NO 443
LENGTH: 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 443, Application US/10505928 Publication No. US20060088532A1 GENERAL INFORMATION:
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
                Sequence 15959, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
  CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                          484 GRAGKVHNFMLGLNLNTS--YPLSPLSDFATQDSFDDDELD--AAVADPD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 FAQKRRRTLDMLIRSLHQDLMPDLHKNMLNRRSFSDVL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 LVRYNQQNDNYRLKIFSEESVPLFGPPLPTPPVFTDHQEFRDFLLVKLINGEKÄTLETPT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 LYXYXQLNDS-----SEEEDEIDGPAGQAEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                             3 GDTPTLHEYMLDLQPETTDLYXYXQLND----SSEEEDEIDGPAGQAEPD
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US/10/953,349
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                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                            Score 53; DB 6;
Pred. No. 1.6e+02;
B; Mismatches 17
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 423;
                                                                                                                                                                                                                                                                                                                        17; Indels
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                                                        CORRESPONDING POLYPEPTIDES
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11222
LENGTH: 288
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3886
LENGTH: 275
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15959
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                                                                  ; ORGANISM: Arabidopsis thaliana US-10-953-349-11222
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US20060105376A1
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 15959
Query Match 10.2%;
Best Local Similarity 27.8%;
Matches 15; Conservative
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CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               44 QAEPDRAHYNIVTFCCKCDSTLRLCVQST---HVDIR-TLEDLLM-----GTLGIVXPIC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 THCCGC
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18; Conserv
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Pred. No. 61;
B; Mismatches
Score 52.5; D
Pred. No. 64;
9; Mismatches
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Pred. No. 22;
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                                                                                                                                                                                                                                                         DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                                 DB
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                                 Length 288;
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19;

Indels

11;

Gaps

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RESULT 56
US-10-525-126-296
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                                                                                           ; ORGANISM: Oryzias latipes
US-10-525-126-296
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US-10-511-937-2561
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US-10-511-937-2561
                                                                                                                                   SEQ ID NO 296
LENGTH: 90
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 296, Application US/10525126
Publication No. US20060093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
Query Match
Best Local Similarity
Matches 13; Conserv
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LENGTH: 1912
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                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 3.2
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SOFTWARE: PatentIn ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 29.6%;
les 16; Conservation
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     version 3.2
                     10.1%;
Score 52; DB Pred. No. 20; B; Mismatches
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Pred. No. 5.1e+02;
9; Mismatches 14;
                                          DB 6; Length 90;
24;
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Indels
20;
Gaps
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Sequence 21799, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND TITLE OF INVENTION: SEQUENCE THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 21799
LENGTH: 324
TYPE: PRT
RESULT 59
US-10-953-349-21798
; Sequence 21798, Application US/10953349
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Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 15960
LENGTH: 97
                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                        l Similarity
17; Conserv
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14; Conserv
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                                                                                             EEKHTEVDLQSSSQSGSLG 171
                                                                                                                                OSTHVDIRTLEDLLMGTLG 88
                                                                                                                                                                   EHKLDWDPTASETKSF----KKHEDLLNDP-
                                                                                                                                                                                                     EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCV
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Pred. No. 22;
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RESULT 61

US-10-953-349-31968
; Sequence 31968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
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US-10-953-349-21797
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 21797
LENGTH: 352
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GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION UNMEER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Pred. No. 90;
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; TYPE: PRT ; ORGANISM: Triticum aestivum US-10-953-349-31966
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31967
LENGTH: 405
TYPE: PRT
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                                                                                                 CURRENT APPLICATION NUMBER: US/11
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31966
LENGTH: 475
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SEQ ID NO 31968
LENGTH: 357
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Query Match
Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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19; Conserv
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10.1%;
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Pred. No.
 Score
Pred.
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Pred. No. 1.1e+02;
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 No ;

    YNHNEGESAPTKFPSGSAVPSVRDVELAGITVM 294

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   DB 6;
1.3e+02;
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                Length 475;
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Sequence 3174, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTION VET. 2.1
SEQ ID NO 3174
LENGTH: 634
TYPE: PRT
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; LENGTH: 507
; TYPE: PRT
; ORGANISM: RVFV GC
US-10-514-462-4
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US-11-293-697-3174
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US-11-293-697-3174
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US-10-514-462-4
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Publication No. US20060088909A1
GENERAL INFORMATION:
                                                                                                                                                Matches
                                                                                                                                                               Query Match
Best Local S
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Best Local Similarity 30.0%;
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CURRENT APPLICATION NUMBER: US/10/514,462
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: 60/381,557
PRIOR FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic TITLE OF INVENTION: Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Emory University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 EVDFVGAAVSCDAAFLNL-TGCYSCNAGARVCLSITSTGTGSLSAHNKD---GSLHIVLP 384
242 E 242
                                                                      183 HEMMEEEEEIPKPKSVVAPPGAPKKEHVNVV-FIGHVDAGKSTIGGQIMYLTGMVDKRTL
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                                     80 E
                                                                                                       29 NDSSEEEDEIDGP----AGQAEPDRAHYNIVTFCCKCD---STL--RLCVQSTHVDIRTL 79
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                                                                                                                                                                 Similarity
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                                                                                                                                            10.1%;
nilarity 34.4%;
Conservative
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Pred. No. 1.7e+02;
9; Mismatches 21;
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Pred. No. 1.4e+02;
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FILE REFERENCE: 050508-2210
CURRENT APPLICATION NUMBER: US/10/514,462
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: 60/381,557
PRIOR FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
SEQ ID NO 2.
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                                  S
                                                                                                                                                            ; NAME/KEY: MOD_RES
; LOCATION: (55)
; OTHER INFORMATION: Variable amino acid
US-10-525-126-302
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US-10-525-126-302
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US-10-514-462-2
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TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH

FILE REFERENCE: 6899-6/PAR

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR TILING DATE: 2003-08-22

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR FILING DATE: 2002-08-22

PRIOR FILING DATE: 2002-08-22

PRIOR FILING DATE: 2002-08-22

PRIOR SEQ ID NOS: 329

SOFTWARE: PATENTIN Ver. 3.2

SEQ ID NO 302

LENGTH: 61
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GENERAL INFORMATION:
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Publication No. US20060088909A1
GENERAL INFORMATION:
APPLICANT: Emory University
TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
TITLE OF INVENTION: Compositions
                                                                                                Query Match
Best Local Similarity
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LOCATION: (37)
OTHER INFORMATION:
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5 TEEVGSIDSPVGEHQQPGGESMRLPEHFRFKRXSHLSLCRWCCNC 49
                                                                               Conservative
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                                                                                                10.0%;
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Pred. No. 15;
8; Mismatches
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Pred. No. 3e+02;
9; Mismatches 2
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RESULT 68 US-10-953-349-6871

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RESULT 70
US-11-297-160-7
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US-10-953-349-6870
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 6870
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6871
LENGTH: 145
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Best Local 9
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Best Local (
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APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Zhan, Qimin
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                           APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such FILE REPERENCE: 015280-367100US
                     CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
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  NUMBER:
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30.4%; Pred. No. 43;
tive 7; Mismatches
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US/10/600,158
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 24841
LENGTH: 315
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24841, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
Sequence 24840, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Best Local :
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: human growth arrest and DNA-damage-inducible OTHER INFORMATION: protein (hGADD45gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                             40 GPAGQAEPDRAHYNIVTFCCKCDST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 MQGAGKALHELLLSAQRQGCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 -- QIHFTLIQAFCCEND 89
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                                                                                                                                                                                                                                                                                                                       5 TPTLHEYMLD------LQPE---TTDLYXYXQLN-------DSSEEEDEID 39
                                                                                                                                                                                                                                                                                                                                                            20;
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Pred. No. 91;
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Pred. No. 43;
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                                          FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252

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Publication No. US20060105914A1

GENERAL INFORMATION:
APPLICANT: TAYLOR, LARRY EDMUND
APPLICANT: HUTCHESON, STEVEN WAYNE
APPLICANT: HUTCHESON, STEVEN WAYNE
APPLICANT: HOWARD, NATHAN A.
APPLICANT: HOWARD, NATHAN A.
APPLICANT: HOWARD, NICHAEL
TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
FILE REFERENCE: 108172-00121
CURRENT APPLICATION NUMBER: US/11/121,154
CURRENT FILING DATE: 2005-04
PRIOR APPLICATION NUMBER: 60/567,971
PRIOR APPLICATION NUMBER: 60/567,971
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US-10-953-349-22956
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; ORGANISM: Glycine max
US-10-953-349-24840
                                                                                                                                                    Sequence 22956, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXAUROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                       NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22956
LENGTH: 155
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 195
 Query Match
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Best Local Similarity
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                                                   ORGANISM: Glycine max
                                                                          TYPE: PRT
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5. US20060105914A1
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   9.9%;
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Pred. No. 1.5e+02;
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   Score 51;
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   DB
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Length 155;
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16871
LENGTH: 549
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-16871
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US-10-953-349-22955
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22955
LENGTH: 171
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16871, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                        Matches
                                                                                                         Query Match
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                                                                                          Local
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478
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                                 22 LYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 SSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQ--STHVDIRTLEDLLMGTL- 87
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                                                                                          Similarity
 LHLSSKLSDDSNVCLDVDD-----NNNIVTNACKCLSRDRTCDPSS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQEQEGGLRDKPGKR----RDHYH----TCYCLSGLSLCQYSWSKHPDSPPLPNLVLGPYS 143
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                                                                      Conservative
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tive 10; Mismatches
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                                                                    Score 51; DB (
Pred. No. 1.9e-
7; Mismatches
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                                                                                          1.9e+02;
                                                                                                           DB 6;
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RESULT 77

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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16869, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16870, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                             NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 4398
                                                                                                                                                                                                                                                                                             Sequence 4398, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16869
LENGTH: 585
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                            APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1579PUS2
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TYPE: PRT
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ORGANISM: Homo sapiens
                                               LENGTH: 764
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ilarity 31.4%;
Conservative
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llarity 31.4%;
Conservative
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Pred. No. 1.9e+02;
7; Mismatches 18
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US-10-953-349-23159
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US-10-953-349-23159
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Best Local S
Matches 18
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 13813
LENGTH: 176
TYPE: PRT
ORGANIGM: Glycine max
                                                                                                                                                                                                                                                                       Sequence 23159, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 23159
LENGTH: 218
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Publication No. US20060107345A1
GENERAL INFORMATION:
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61 LIDTAGCOMEEKKÖEEDSTFNEGEAE---
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                                                                                                           1 MHGDTPT-----LHEYMLD------LQPETT-----DLYXYXQLN-----
                                                                                                                                                                    Similarity
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                                   -----DSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLED 81
                                                                        MYGDEITSMLTIQYRMHELIMDWSSKELYNSKIKAHPSVTAHMLYDLEGVKRTNSTEPTL 60
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25.0%; Pred. No. 62;
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Pred. No. 2.7e+02;
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Pred. No. 79;
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 -VTVTHAKRLVQSG 100
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US-10-953-349-23158
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; LENGTH; 235
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-36029
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US-10-953-349-23158
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publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERBENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 23158
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 34
TYPE: PRT
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Local Similarity 28.6%;
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Similarity 19.3%; Pred. No. 1.3e+02;
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Pred. No. 85;
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RESULT 86

US-10-953-349-9399

; Sequence 9399, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-99-30
; NUMBER OF SEQ ID NOS: 40252
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US-10-953-349-23157
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TITLE OF INVENTION: SEQUENCE-DEFERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23157
LENGTH: 382
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PAPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 36028
LENGTH: 369
TYPE: PRT
ORGANISM: Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        225 LLIDTAGCDMEEKKDEEDSTFNEGEAE---
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Pred. No. 1.
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Pred. No. 1.4e+02;
9; Mismatches 20;
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                                                                                                             DNA FRAGMENTS
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1.5e+02;
hes 37;
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; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27383
; LENGTH: 205
; TYPE: PRT
; ORGANIEM: Triticum aestivum
US-10-953-349-27383
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 9398
LENGTH: 81
TYPE: PRT
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Publication No. US20066107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY
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SEQ ID NO 9399
LENGTH: 57
 Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Local Similarity 24.6%;
Les 15; Conservative
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ilarity 24.6%;
Conservative
 9.7%;
21.3%;
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Score 50;
Pred. No.
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 DB
84;
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                Length 205;
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CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38511
LENGTH: 211
TYPE: PRT
ORGANISM: Zea mays subsp. mays
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version
SEQ ID NO 27382
LENGTH: 231
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Triticum aestivum
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93 VDRILYSSVVYPHNYGFVPRTLCEDGDPIDVLVL 126
                                  47 PDRAHYNIVTFCCKCDSTLR-LCVQSTHVDIRTL 79
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                                                                                                                                                                  Similarity
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                                                                     DAPKLNORMVSSLSKRTAAAHSWHDLEIGPEAPLIFNAVVEITKGSKVKYELDKKTGMIK 92
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Pred. No.
                                                                                                                                                                Score 50; DB 6; Length 231; Pred. No. 95;
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FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR PRIOR PILING DATE: 2003-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR PILING DATE: 2002-04-24

PRIOR PILING DATE: 2002-04-27

PRIOR PILING DATE: 2002-04-27

PRIOR PRIOR PILING DATE: 3002-04-29

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: PATENTIN VETSION 3.2

SEQ ID NO 2618
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US-10-511-937-2618
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                                                                                                                                                                                                                                                          Sequence 12546, Application US/10953349
Publication No. U320060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 12546
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 27
TYPE: PRT
                                                                                                                                                                                                                          TYPE: PRT
                                                                                                           Match 9.7%;
Local Similarity 28.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 LKM 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 HDYALPVGKQKQDLL-
                                         17 PETTDLYXYXQLNDSSEEED----EIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 LRL 67
                                                                                                                                                                                                                                               293
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PENTSL-----DRNNEKNAGMVEFVSPNGE-----VFICKSDLELGLCHODK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woodward, Robert
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                                                                                        Conservative
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                                                                      Score 50; DB 6; Lengu: ....
Pred. No. 1.2e+02;
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Pred. No. 1.1e+02;
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US-10-953-349-38510
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38510
LENGTH: 343
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8835
LENGTH: 438
TYPE: PRT
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Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                                                                  Best
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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                                                                                                                                                             Local Similarity
les 19; Conserv
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les 17; Conservative
                                                                               118 LSVEMPEIEFARALDDAEEAIFYRHFKPEVVWKMQRLIGVGAELKLKRAHAIFDRVCSKC 177
178 IASKRDEI-SQGIDSSSSKDLLMSSINV 204
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                                       62 DSTLRLCVQSTHVDIRTLEDLLMGTLGI 89
                                                                                                                     15 LOPETTDLYXYXQLNDSSE------EEDEIDGPAGQAEPDRAHYNIVTFCCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 GQAEPD-----RAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXP 92
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                                                                                                                                                               Conservative
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                                                                                                                                                                             9.7%; Score 50; DB 6;
21.6%; Pred. No. 1.9e+02;
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Pred. No. 1.5e+02;
7; Mismatches 27;
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RESULT 95 US-10-953-349-8834 ; Sequence 8834, Application US/10953349

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RESULT 96
US-10-953-349-8833
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US-10-953-349-13398
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                                                       Sequence 13398, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8833
LENGTH: 516
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SOFTWARE: PatentIn version
SEQ ID NO 8834
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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Pred. No. 2.3e+02;
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Pred. No.
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FEATURE:

NAME/KEY: misc_feature

LOCATION: (30)...(30)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid us-10-953-349-13397
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa can be any naturally occurring amino
US-10-953-349-13398
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                                                                                                                                                                                   RESULT 99
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                  Sequence 13396, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13397
LENGTH: 548
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SEQ ID NO 13398
LENGTH: 527
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Best Local Similarity
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Best Local Similarity
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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                                                                                                                                                                                                                                                                                                                           361 EVNKOKTSADOSOLAESGKKOPFVRRQELLIKSGLADSLLDICIESVGELIRSNLGKEVL 420
                                                                                                                                                                                                                                             421 YEVATGGSDGIMHPVLDDK 439
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                                                                                                                                                                                                                                                                                     79 LEDLIMGTIGIVXPICSOK 97
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CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: PatentIn version 3.3

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Sequence 3814, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEl full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3814
LENGTH: 878
TYPE: PRT
Search completed: May 27, 2006, 05:38:15 Job time: 8.69076 secs
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TYPE: PRT
CORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (116).(116)
THER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13396
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US-11-293-697-3814
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US-11-293-697-3814
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Best Local S
Matches 25
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LENGTH: 634
                                                                                                                                                                                                                                                                              / Match 9.7%; Score 50; DB 7; Length 878;
Local Similarity 24.3%; Pred. No. 4.1e+02;
1es 25; Conservative 15; Mismatches 39; Indels
                                                                                        591 TPELSADELPODIANEIADIPHOLELNQEDFSDVLPRLPDDLQDFDFFEGKNGDLLPTTE 650
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